

# STIC Search Report Biotech-Chem Library

STIC Database Tracking Number: 108396

TO: Sheridan Swope

Search Notes

Location: CM1/12S12&10D)1

Art Unit: 1652 170001

Tuesday, November 25, 2003

Case Serial Number: 09/607745

From: Barb O'Bryen

**Location: Biotech-Chem Library** 

CM1-6A05

Phone: 308-4291

BAB

barbara.obryen@uspto.gov

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### ∠STIČ-Biotech/ChemLib

From:

Sent:

Swope, Sheridan Monday, November 17, 2003 12:48 PM

To: Subject: STIC-Biotech/ChemLib

09607745

For 09607745, pls do the following searches and alignments:

#### Search:

SID 2 against the NT and AA data bases. SID 9 against the NT and AA data bases.

Align SID 2 and 9 with: **EMBL** Acc# AF179224 EMBL Acc# AF216312. EMBL Acc# Q9NRS4 GENSEQ Acc# AAY99417

#### THANKS!!!

Sheridan Swope, Ph.D. Patent Examiner, AU 1652 Recombinant Enzymes sheridan.swope@uspto.gov 703-305-1696 (voice) 703-308-3014 (FAX) Mailbox: CM1 Rm10D01 Office: CM1 Rm12D12

Searcher:
Phone:
Location:
Date Picked Up:
Date Completed:
Searcher Prep/Review:
Clerical:
Online time:

TYPE OF SEARCH:
NA Sequences:
AA Sequences:
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:
Other:

VENDOR/COST (whei	re applic.)
STN:	
DIALOG:	
Questel/Orbit:	
DRLink:	
Lexis/Nexis:	
Sequence Sys.:	
www/Internet:	
Other (specify):	

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5.1.6
Compugen Ltd
GenCore version (c) 1993 - 2003
           Copyright
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using sw model - protein search, OM protein

Run

2003, 13:51:12 November 25 :uo

(without alignments)
378.015 Million cell updates/sec

US-09-607-745-2

Title:

2342 1 MDPDSDQPLNSLDVKPLRKP.....VYTKVSAYLNWIYNVWKAEL 435 score: Sequence: Perfect

BLOSUM62 Gapop 10.0 Scoring table:

Gapext 0.5

of hits satisfying chosen parameters: Total number

residues

2 seqs, 869

Searched:

N

seq length: 0 seq length: 2000000000 Minimum DB Maximum DB

Maximum

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

aa.pep:\* Database

chance to have a result being printed Pred. No. is the number of results predicted by chance to h score greater than or equal to the score of the result bein and is derived by analysis of the total score distribution.

## SUMMARIES

sult Query No. Score Match Length DB ID Description	TOIG of: g9nrs4 TOIG of: aay9941
CI	2337 99.8 437 1 g9nrs4 2297.5 98.1 432 1 aay99417
DB	
Length	432
Query Match Length DB	99.8
tesult No. Score	2337 2297.5
Result No.	Н И

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, Last sequence update)
, Last annotation update)
se, serine 4 (EC 3.4.21.-) (Membrane-type serine
                                                                                                                 Chordata; Craniata; Vertebrata; Euteleostomi;
Primates; Catarrhini; Hominidae; Homo,
                           437 AA
         from: 1 to: 437
                                                Created)
         316
                           STANDARD;
                                 Q9NKS4; Q9NZA5;
16-OCT-2001 (Rel. 40, C
16-OCT-2001 (Rel. 40, I
15-SEP-2003 (Rel. 42, I
Transmembrane protease,
protease 2) (MT-SP2).
                                                                                             TMPRSS3.
                                                                                                       Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
         check
                                                                                     protease 2)
TMPRSS4 OR I
        TOIG of: q9nrs4
                           HUMAN
q9nrs4
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NCBI\_TaxID=9606;

MEDLINE=20283276; PubMed=10825129;
Wallrapp C., Haehnel S., Mueller-Pillasch F., Burghardt B.,
Iwamura T., Ruthenbuerger M., Lerch M.M., Adler G., Gress T.M.;
"A novel transmembrane serine protease (TMPRSS3) overexpressed in pancreatic cancer.";
Cancer Res. 60:2602-2606(2000).

TISSUB-Pancreas;

XX STURNE-22388257; PubMed=12477932;

XX STURNE-22388257; PubMed=12477932;

XX Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

XX Klausner R.D., Collins F.S., Magner L., Shenmen C.M., Schuler G.D.,

XX Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

XX Diatchenko L., Marusina K., Farner A.A., Rubin G.M., Hong L.,

XX Diatchenko L., Marusina K., Paramer A.A., Rubin G.M., Hong L.,

XX Diatchenko L., Marusina K., Paramer A.A., Rubin G.M., Hong L.,

XX Branstein M.J., Usdin T.B., Toshiyuki S., Carninol P., Willahy S.J.,

XX Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

XX Bans S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

XX Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

XX Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

XX Holards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

XX Hards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

XX Hands J., Would A., Youdman M., Madan A., Rodrigues S., Sanchez A.,

XX Haley J., Helton E., Kerman M., Madan A., Rodrigues S., Sanchez A.,

XX Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

XX Blakesley R.W., Touchman J.W., Green E.D., Myers R.M.,

XX Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

XX Generation and initial analysis of more than 15,000 full-length

XX Generation and initial analysis of more than 15,000 full-length

XX Fuman and mouse cDNA sequences ";

YX Generation And Intial Analysis of more than 15,000 full-length

YX GASTROINESTHAM A ROLE IN TWOR PROGRESSION,

XX FORMATION AND TUWOR INVASION.

XX FORMATION AND TUWOR INVASION.

XX FORMATICAN AND TUMOR INVASION.

XX FORMATILARY CANCER. VERY WEAK EXPRESSION IN NORMAL.

XX FORMATITY: Contains 1 SRCR domain.

XX FORMATICAL COLTAINS 1 LDL-receptor class A domain. SEQUENCE FROM N.A.
Smeekens S.S., Lorimer D.D., Wang E., Hou J., Linnevers C.;
"MT-SP2, a novel type II membrane serine protease expressed in trachea, colon, and small intestine: identification, cloning, chromosomal localization.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases. FROM

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).

GO; GO:0016021; C:integral to membrane; NAS.
GO; GO:0016021; C:integral to membrane; NAS.
GO; GO:0006508; P:proteolysis and peptidolysis; NAS.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001272; LDL\_receptor\_A.
InterPro; IPR001294; Ser\_protease\_Try.
InterPro; IPR00190; Srcr\_receptor.
Pfam; PF00057; Idl\_recept\_a; 1.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00122; CHYMOTRYPSIN.
SMART; SM00192; LDLa; 1.
SMART; SM00202; SR; 1.
SMART; SM00202; SR; 1.
SMART; SM00209; LDLA; 1.
SMART; SM00209; LDLA; 1.
SMART; SM00209; LDLRA\_2; FALSE\_NEG.
PROSITE; PS00420; SRCR\_1; FALSE\_NEG.
PROSITE; PS0287; SRCR\_2; 1.
PROSITE; PS0287; SRCR\_2; 1. EMBL; AF179224; AAF74526.1; -... EMBL; AF216312; AAF31436.1; -... EMBL; BC011703; AAF11703.1; -... HSSP; P00763; 1DPO... MEROPS; S01.034; -... Genew; HGNC:11878; TMPRSS4. Genew; How. "TM: 606565; -.

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10-SEP-1998;
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SERIAL SYSTEM (BY SIMILARITY).
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CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CLEAVAGE (POTENTIAL).
BY SIMILARITY.
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AHCFRKHTDVFNWKVRAGSDKLGSFPSLAVAKIIIIEFNPMYPKDNDIALMKLQFPLTFS
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                                                                                        (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
LDL-RECEPTOR CLASS A.
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to: 432

from: 1 432 AA

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Human; PRO polypeptide; membrane bound protein; receptor; diagnosis; transmembrane; secretion; immunoadhesion; pharmaceutical; screening.
Human PRO1570 (UNQ776) amino acid sequence SEQ ID NO:275
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980'S-0100664.

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980'S-0100919.

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28-SEP-1998;

29-SEP-1998;

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The
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                                                                                               AAA37022 to AAA37144 encode the new isolated human transmembrane, receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The transmembrane and receptor PRO proteins can be used for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions. The polypeptides and nucleotide sequences encoding then have various industrial applications, including uses as pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR primers and hybridisation probes used in the isolation of the PRO polypeptides from the present invention.
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               New mammalian DNA sequences encoding transmembrane, receptor or secreted PRO polypeptides, useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions
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253.748 Million cell updates/sec
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(c) 1993 - 2003 Compugen Ltd
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Pred. No. 0;
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Best Local Similarity 98.8%;
Matches 429; Conservative 0
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US-09-607-745-9

Title:

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TOIG of: g9nrs4
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            .....LNWIYNVWKAELSRHHHHHH 292
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1; immunoadhesion; pharmaceutical;
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tch 100%
rst 45 summaries
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q9nrs4
1600
1 MDSKGSSQKSRLLLLLVVSN...
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                                          Gapext 0.5
                                                             residues
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98US-0098749.

98US-0098750.

98US-0098821.

98US-0098843.

98US-0099536.

98US-0099596.

98US-0099596.

98US-0099598.

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Maximum DB seq length: 2000000000
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transmembrane; secretion
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Match Length I
                              BLOSUM62
Gapop 10.0 ,
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                                                             2 segs, 869
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Maximum Mat
Listing fir
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01-SEP-1998;
02-SEP-1998;
02-SEP-1998;
02-SEP-1998;
09-SEP-1998;
09-SEP-1998;
09-SEP-1998;
09-SEP-1998;
10-SEP-1998;
10-SEP-1998;
10-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                               Scoring table:
Perfect score;
Sequence:
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                                                                                Total number
                                                                                                                                                                         Database :
                                                             Searched:
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No.
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        PR
        10-SEP-1998;
        98US-0099808.

        PR
        10-SEP-1998;
        98US-0099812.

        PR
        10-SEP-1998;
        98US-0099812.

        PR
        10-SEP-1998;
        98US-0099812.

        PR
        15-SEP-1998;
        98US-0099816.

        PR
        15-SEP-1998;
        98US-0009816.

        PR
        15-SEP-1998;
        98US-0100389.

        PR
        15-SEP-1998;
        98US-0100384.

        PR
        15-SEP-1998;
        98US-0100664.

        PR
        16-SEP-1998;
        98US-0100664.

        PR
        17-SEP-1998;
        98US-0100664.

        PR
        27-SEP-1998;
        98US-0101477.

        PR
        23-SEP-1998;
        98US-0101477.

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        23-SEP-1998;
        98US-0101474.

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RC TISSUE=Pancreas;

KE SENGENCE FROM N.A.

REASTRONGE FROM N.A.

REASTRONGE FROM N.A.

REASTRONGE FROM N.A.

KITAUSDES R.L., Feathgold B.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Blacklehako L., Marushia K., Farmer A.A., Rubin G.W., Hong L.,

Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Rahas S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Willalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

RA Willalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

RA Willalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rabacsley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Multing M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Generation and initial analysis of more than 15,000 full-length

RI human and mouse cDNA sequences.",

ROCALTION: MAY PLAY A ROLE IN TUMOR PROGRESSION, METASTASIS

FORMATION AND TUMOR INVASION.

-I- FUNCTION: MAY PLAY A ROLE IN TUMOR PROGRESSION, METASTASIS

C-- FUNCTION: MAY PLAY A ROLE IN TWOR PROGRESSION IN NORMAL

AND AMPULLARY CANCER. VERY WEAK EXPRESSION IN NORMAL

GASTROINTESTINAL AND URGENITAL TRACT.
            259 KLGSFPSLAVAKIIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFDEELTPATP 318
                                                                                                                                                                                                                                                                                                                                                                                                         TMS4 HUMAN
Q9NRS4; Q9NZA5;
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
Transmembrane protease, serine 4 (EC 3.4.21.-) (Membrane-type serine Transmembrane protease)
                                                                                                                 LWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPEGGVDTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wallrapp C., Haehnel S., Mueller-Pillasch F., Burghardt B.,
Iwamura T., Ruthenbuerger M., Lerch M.M., Adler G., Gress T.M.;
"A novel transmembrane serine protease (TMPRSS3) overexpressed in
                                                                                                                                                                                                       QGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL 432
                                                                                                                                                                          QGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Smeekens S.S., Lorimer D.D., Wang E., Hou J., Linnevers C.; "MT-SP2, a novel type II membrane serine protease expressed in trachea, colon, and small intestine: identification, cloning, echromosomal localization."; Submitted (DEC-1999) to the BMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                   to: 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUE=Pancreatic carcinoma;
MEDLINE=20283276; PubMed=10825129;
                                                                                                                                                                                                                                                                                                                                                                 from: 1
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Best Local Similarity 97.4%
Matches 228; Conservative
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polypeptides from the
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
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LDL-RECEPTOR CLASS A.
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CLEAVAGE (POTENTIAL)).
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N-LINKED (GLCNAC. . . .
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
-!- SIMILARITY: Contains 1 SRCR domain.
-!- SIMILARITY: Contains 1 LDL-receptor class A
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MEROPS; S01.034; -... Genew; HGNC:11878; TMPRSS4.

MIM; 606565; -... GOS CO16021; C:integral to me GO; GO:0016021; C:integral to me GO; GO:0016021; C:integral to conterpro; IPR001314; Chymotrypsi InterPro; IPR001314; Chymotrypsi InterPro; IPR001314; Chymotrypsi InterPro; IPR001254; Ser_proteas InterPro; IPR001254; Ser_proteas InterPro; IPR001254; Ser_proteas InterPro; IPR001254; Ser_proteas InterPro; IPR00125; LDLa; 1... PR00182; LDLa; 1... SMART; SM00202; SR; 1... SMART; SM00202; SR; 1... SMART; SM00202; SR; 1... SMART; SM00202; SR; 1... PROSITE; PS50040; IDLRA_2; FALSE PROSITE; PS50040; TRYPSIN_HIS; 1 PROSITE; PS50040; TRYPSIN_HIS; 1 PROSITE; PS00134; TRYPSIN_HIS; 1 Hydrolase; Serine protease; Transomen 39 59 59
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KIVGGYALDVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHCFRKHTDVFNWKVRAGSD 110

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204 RVVGGEBASVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHCFRKHTDVFNWKVRAGSD 263
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SIIIVVVLIKVILDKYŸFLCGQPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAV
AVRLSKDRSTLQVLDSATGNWFSACFDNFTEALAETACRQMGYSSKPTFRAVEIGPDQ
DLDVVEITENSQELRMRNSGPCLSGSLVSLHCLACGKSLKTPRVVGGEEASVDSWPW
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IIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFDEELTPATPLWIIGWGFTKQ
NGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPEGGVDTCQGDSGGPLM
               1 (bases 1 to 2081)
Wallrapp, C., Hahnel, S., Muller-Pillasch, F., Burghardt, B.,
Iwamura, T., Ruthenburger, M., Lerch, M.M., Adler, G. and Gress, T.M.
A novel transmembrane serine protease (TMPRSS3) overexpressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein_id="AAF74526.1"
'db_xref="G1:8347149"
'translation="MLQDPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPIIIALL
                                                                                                                                                                       2 (bases 1 to 2081)
Wallrapp,C. and Gress,T.M.
Direct Submission
Submitted (20-AUG-1999) Internal Medicine I, University of Ul
Robert-Koch-Street 8, Ulm, Baden-Wuerttemberg 89081, Germany
Location/Qualifiers
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo
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308. .373
/gene="TMPRSS3"
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Cancer Res. 60 (10), 2602-2606 (2000)
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order(800. .802,1142. .1144)
/gene="TMPRSS3"
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/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="11"
/map="11q23.3"
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order(902, .904,950, .952)
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/product="transmembrane
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/gene="TMPRSS3"
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/note="disulfide bond"
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/gene="TMPRSS3"
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/gene="TMPRSS3"
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gene="TMPRSS3"
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/gene="TMPRSS3"
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/gene="TMPRSS3"
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/gene="TMPRSS3"
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/gene="TMPRSS3
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Homo sapiens transmembrane serine protease 3 (TMPRSS3) mRNA, complete cds.

AF179224

AF179224.1 GI:8347148
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-WODEL=frame+_p2n.model -DEV=soft -Q=US09607745.pep -DB=nt.seq -SUFFIX=pto
-OUT=nacompare.res -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1
-BND=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200
-THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -NCPU=6 -NO_XLDXY
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -NCPU=6 -NO_XLDXY
-NGG_SCORES=0 -LONGLOG -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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TOIG of: af21631
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TOIG of: af21631
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                                                                                                                             2003, 13:57:34; Search time 1.79505 Seconds (without alignments)
2.016 Million cell updates/sec
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1 MDPDSDQPLNSLDVKPLRKP......VYTKVSAYLNWIYNVWKAEL
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Compugen Ltd
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Submitted (14-DEC-1999) Axys Pharmaceuticals, Inc, 180 Kimball Way, South San Francisco, CA 94080, USA
Location/Qualifiers
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1 (bases 1 to 2079)
Smeekens; S.S., Lorimer, D.D., Wang, E., Hou, J. and Linnevers, C.
MT-SP2, a novel type II membrane serine protease expressed in trachea, colon, and small intestine: identification, cloning, and chromosomal localization
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                                    1184 CTCTGGAFCATTGGAFGGGGCTTTACGAAGCAGAATGGAGGAAGATGTCTGACATACTG 1243
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GlyThrValArgProlleCysLeuProPhePheAspGluGluLeuThrProAlaThrPro 321
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Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 2081)

Wallrapp, C., Hahnel, S., Muller-Pillasch, F., Burghardt, B.,

Iwamura, T., Ruthenburger, M., Lerch, M.M., Adler, G. and Gress, T.M.

A novel transmembrane serine protease (TMPRSS3) overexpressed in pancreatic cancer

Cancer Res. 60 (10), 2602-2606 (2000)

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Direct Submission
Submitted (20-AUG-1999) Internal Medicine I, University of Ulm, Robert-Koch-Street 8, Ulm, Baden-Wuerttemberg 89081, Germany Location/Qualifiers
  oLeuTrpIleIleGlyTrpGlyPheThrLysGlnAsnGlyGlyLysMetSerAspIleLe
                                                                                                                                                GCTGCAGGCGTCAGTCCAGGTCATTGACAGCACACACGGTGCAATGCAAGACGATGCGTACCA
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Homo sapiens transmembrane serine protease 3 (TMPRSS3) complete cds.
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Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2079)

Smeekens, S.S., Lorimer, D.D., Wang, E., Hou, J. and Linnevers, C.

MT-SP2, a novel type II membrane serine protease expressed in trachea, colon, and small intestine: identification, cloning, and chromosomal localization

L Unpublished

E (bases 1 to 2079)

Smeekens, S.S., Lorimer, D.D., Wang, E., Hou, J. and Linnevers, C.

Direct Submission

L Submitted (14-DEC-1999) Axys Pharmaceuticals, Inc, 180 Kimball Way, South San Francisco, CA 94080, USA

Location/Qualifiers
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                                                                                                                                                                                                                                                                   uLeuArgMetArgAsnSerSerGlyProCysLeuSerGlySerLeu
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(without alignments)
2.016 Million cell updates/sec
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            Check:
            Type: N
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- 2003 Compugen Ltd
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                                                         Length:
Matches:
Conservative:
Mismatches:
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(c) 1993
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835 CTCCCACCCACCA
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703 AACAACATCCAGA
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Job time: 5.79505 secs
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Best Local Similarity:
Query Match:
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Minimum DB seq length: 0 Maximum DB seq length: 20000

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2 segs, 4160

Searched:

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1 (bases 1 to 2079)
Smeekens, S.S., Lorimer, D.D., Wang, E., Hou, J. and Linnevers, C.
MT-SP2, a novel type II membrane serine protease expressed in trachea, colon, and small intestine: identification, cloning, and chromosomal localization
Unpublished
2 (bases 1 to 2079)
Smeekens, S.S., Lorimer, D.D., Wang, E., Hou, J. and Linnevers, C.
Direct Submission
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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TOIG of: af17922
TOIG of: af21631
TOIG of: af17922
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Submitted (14-DEC-1999) Axys Pharms
South San Francisco, CA 94080, USA
Location/Qualifiers
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Match 100%
first 45 summaries
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AF216312
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Homo sapiens
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                                   Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi,
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 2081)
Wallrapp,C., Hahnel,S., Muller-Pillasch,F., Burghardt,B.,
Iwamura,T., Ruthenburger,M., Lerch,M.M., Adler,G. and Gress,T.M.
A novel transmembrane serine protease (TMPRSS3) overexpressed in
pancreatic cancer
Cancer Res. 60 (10), 2602-2606 (2000)
                                                                                                                                                                                                                                              Localian

2 (bases 1 to 2081)

Wallrapp,C. and Gress,T.M.

Direct Submission

Submitted (20-AUG-1999) Internal Medicine I, University of Ulm,

Robert-Koch-Street 8, Ulm, Baden-Wuerttemberg 89081, Germany

Location/Qualifiers
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                         VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1358 CAGGGTGACAGTGGTGGGCCCCTGATGTACCAATCTGACCAGTGGCATGTGGTGGGCATC
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                                                                                     Type: N
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728
                                                                                                                                              Length:
Matches:
Conservative:
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1266.00
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/codon_start=1
/product="type II membrane serine protease"
/product="type II membrane serine protease"
/protein_id="AAF31436.1"
/db_xref="GI:6911219"
/translation="MSNPCANPVSPWRPSESVGIPIIIALLSLASIIIVVVLIKVILD
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RMRNSSGPCLSGSLVSLHCLACGKSLKTPRVVGGEBASVDSWPWQVSIQYDKQHVCGG
SILDPHWVLTAAHCFRKHTDVFNWKVRAGSDKLGSFPSLAVAKIIIIEFNPMYPKDND
IALMKLQFPLTFSGTVRPICLPFFDEELTPATFLWIIGWGFTKQNGGKMSDILLQASV
QVIDSTRCNADDAYQGEVTEKMMCAGIPEGGVDTCQGDSGGPLMYQSDQWHVVGIVSW
GYGGGGFSTPGVYTKVSAYLMWIYNVWKAEL"
                                                                                              Craniata, Vertebrata, Euteleostomi,
Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                           E 2 (bases 1 to 2079)
S Smeekens, S.S., Lorimer, D.D., Wang, E., Hou, J. and Linnevers, C.
Direct Submission
L Submitted (14-DEC-1999) Axys Pharmaceuticals, Inc, 180 Kimball W.
South San Francisco, CA 94080, USA
Location/Qualifiers
1. .2079
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
251. .1522
                                                                                                                                                                                                                                                            180 Kimball
                                                                             Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostc
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2079)
Smeekens, S.S., Lorimer, D.D., Wang, E., Hou, J. and Linnevers, C.
MT-SP2, a novel type II membrane serine protease expressed in
trachea, colon, and small intestine: identification, cloning,
Unpublished
         complete
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AF216312.1 GI:691121
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ABU72164 ABU65733 ABU66066 ABU67570 ABU65428 ABU58564

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Human; seripancrin; serine protease; chromosome 11q22-q23; therapy; arthritis; chronic obstructive pulmonary disorder; COPD; cancer; osteoporosis; aberrant wound healing; angiogenesis; diabetes; inflammatory disorder; stroke; cardiovascular disease; gene therapy; vaccine; cytostatic; cerebroprotective; vulnerary; osteopathic.
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ALIGNMENTS

Matzku 04-JUL-2000; 2000WO-EP06211. 99EP-0113428 Suendermann B, Hofmann U, (MERE ) MERCK PATENT GMBH

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Wilbert

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care;

Serine protease; D-G; human; zymogen; enzyme; cytostatic; antiinflammatory; dermatological; anticoagulation; cancer; skin disorder; neuropathic pain; inflammatory disorder; coagulation diathesis; thrombosis; laundry detergent; skin

gene therapy

serine protease D-G amino acid sequence.

ine protease Seripancrin, useful for treating arthritis, chronic obstructive pulmonary disease, disorders, stroke, angiogenesis and aberrant

45pp; English

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The present invention relates to seripancrin polynucleotides, and polypeptides encoded by them. Seripancrin are members of serine protease family. This protein contains a transmembrane domain, a low density lipoprotein (LDL) domain, protease domain and a scavenger receptor cysteine-rich (SRCR) domain. The LDL and SRCR domains help to define the specificity of seripancrin's intra and intermolecular interactions. The polynucleotides and polypeptides of the invention are useful for treating and diagnosing diseases such as arthritis, chronic obstructive pulmonary disorder (COPD), cancer, osteoporosis, aberrant wound healing, angiogenesis, inflammatory disorders, diabetes, stroke and cardiovascular diseases. Seripancrin genes are useful in chromosome localisation studies, as tools for tissue expression studies and also in gene therapy. The polypeptides of the invention are used for identifying agonists and antagonists useful for treating conditions associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                   as tools for tissue expression studies and also in gene therapy. The polypeptides of the invention are used for identifying agonists and antagonists useful for treating conditions associated with seripancrin imbalance. These polypeptides are also useful as vaccines. The present sequence is seripancrin protein. The seripancrin gene is located on human chromosome 11q22-q23.
                           extracellular serine
                                                 cancer, osteoporosis, diabetes, inflammatory wound healing -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               435 AA;
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Best Local Similarity 100.
Matches 435; Conservative 딢 WFSACFDNFTEAL MDPDSDQPLNSLD LCGOPLHFIPRKO SAYLNWIYNVWKA CLSGSLVSLHCLA SAYLNWIYNVWKA WFSACFDNFTEAL CLSGSLVSLHCLA AAHCFRKHTDVFN AAHCFRKHTDVFN SGTVRPICLPFFD SGTVRPICLPFFD QGEVTEKMMCAGI OGEVTERMMCAGI 421 181 241 241 301 301 361 421 361 셤  $\stackrel{\sim}{\circ}$ 셤 à d 8 ò

The invention relates to an isolated and purified nucleic acid that encodes a serine protease called D-G protein. The activity of the protein of the invention may be described as cytostatic, antiinflammatory, dermatological and anticoagulation. The serine protease of the invention is a member of the trypsin/chymotrypsin-like (S1) serine protease family, which play an important role in processes such as digestion and regulatory amplification cascades through the proteclytic activation of regulatory amplification escades through the proteclytic activation of inactive zymogen precursors. Protease D-G modulating compounds are useful for treating a condition which is mediated by protease D-G, e.g. cancer, skin disorders, neuropathic pain, inflammatory disorders, or coagulation diathesis/thrombosis. The polynucleotide encoding the protease is useful for identifying modulators of the functional protease. The D-G protein can be used for formulation of compositions for laundry detergents and skin care products. Protease D-G gene therapy may be used to introduce protease D-G into the cells of target organisms. As the D-G protein is servived from a human, it is less likely to produce an allergic reaction in sensitive individuals when used current sequence represents the human serine protease D-G amino acid 202..203 - residues spanning the zymogen cleavage site" i S Nucleic acid encoding a serine protease called D-G protein which useful for identifying modulators that are useful for treating a condition which is mediated by protease D-G, e.g. cancer, skin disorders, or neuropathic pain -31..52 /note= "hydrophobic transmembrane domain" 'note= "catalytic triad residue" residue" /note= "catalytic triad 361 385 /note= "catalytic triad "Encoded by CTG" <u>ц</u> Jocation/Qualifiers Andrade-Gordon Claim 13; Fig 1B; 81pp; English. (ORTH ) ORTHO-MCNEIL PHARM INC 08-JUN-2001; 2001WO-US18568. 30-JUN-2000; 2000US-0607745. 'note= 93 WPI; 2002-106601/14 Qi J, N-PSDB; AAI64284. Misc-difference WO200202011-A1 sapiens 10-JAN-2002. Active-site Active-site Active-site Darrow AL, Region Ношо 

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                                                                                                                                                                The invention describes a purified polypeptide, which comprises a fragment of a kinase, phosphatase, protease, protease inhibitor, transporter, cytoskeletal protein, receptor or transcription factor. The polypeptide is useful as an immunogenic composition for eliciting in a mammal an immunogenic response directed against any of the purified polypeptide, or the antibody that binds to this polypeptide, is useful for treating cancer. The polypeptide is also useful for identifying compounds that binds to a naturally processed class I or class II MHC-binding polypeptide. The polypeptides and polynucleotides are particularly useful for treating or preventing myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma, lymphoma or leukaemia. These are also useful for screening agents for treating the above mentioned diseases. This sequence represents an expressed protein tag (BPT) isolated from human tissue for translational
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Note: This sequence does not appear in the printed specification but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
           cytoskeletal proteins, receptors or transcription factors), useful for treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or leukemia
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Pred. No. 3.3e-194;
Mismatches 0; I
(e.g. kinases, phosphatases,
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Best Local Similarity 100.0%; P. Matches 435; Conservative 0;
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240

300 300 360

420 360

420

28-MAR-2002;

10-OCT-2002

28-MAR-2001;

Homo sapiens

leukaemia

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CLSGSLVSLHCLACGKSLKTPRVVGGEEASVDSWPWQVSIQYDKQHVCGGSILDPHWVLT
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inflammation;
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176
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303
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148
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Modified-site
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     tag (EPT)
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99.8%; Pred. No. 7.3e-194;
ive 1; Mismatches 0;
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              "characteristic
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Matches 434; Conser
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The invention describes a purified polypeptide, which comprises a fragment of a kinase, phosphatase, protease, protease inhibitor, transporter, cytoskeletal protein, receptor or transcription factor. The polypeptide is useful as an immunogenic composition for eliciting in a mammal an immunogenic response directed against any of the purified polypeptide, or the antibody that binds to this polypeptide, is useful for treating cancer. The polypeptide is also useful for identifying compounds that binds to a naturally processed class I or class II MHC-binding polypeptide. The polypeptides and polynucleotides are particularly useful for treating or preventing and polynucleotides are particularly useful for treating or preventing myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma, I myeloma or leukaemia. These are also useful for screening agents for treating the above mentioned diseases. This sequence represents an expressed protein tag (BPT) isolated from human tissue for translational
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Pred. No. 7.3e-194;
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21-MAY-2001; 2001US-292544P.
08-AUG-2001; 2001US-310801P.
01-OCT-2001; 2001US-326370P.
04-DEC-2001; 2001US-336780P.
20-FEB-2002; 2002US-358985P.
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                                                                                                                                              WFSACFDNFTEALAETACROMGYSSKPTFRAVEIGPDODLDVVEITENSOELRMRNSSGP
                                                                                                                                                                     CLSGSLVSLHCLACGESLKTPRVVGGEEASVDSWPWQVSIQYDKQHVCGGSILDPHWVLT
                                                                                                                                                                                                                                                                                                                                                                                                                                PEGGVDICQGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKV
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                                                                                                                                                                                                                       CGKSLKTPRVVGGEBASVDSWPWQVSIQYDKQHVCGGSILDPHWVLT
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                                                                                                                                                                                                                                                                                                                                                                                    301 SGTVRPICLPFFDEELTPATPLWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAY
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"Transmembrane domain"
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            MDPDSDQPLNSLD
                                                                                LCGOPLHFIPRKO
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06-SEP-2000; 2000US-06.
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N-PSDB; AAI72976.
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(GISH/) GISH K C.
(WILS/) WILSON K E.
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The sequences given in AAG79356-59 show the colorectal cancer proteins, CGA7 and CJA8 proteins are colorectal cancer modulating proteins and have been mapped to chromosomes 2 (CGA7) and 11 (CJA8). These sequences may be used in the method of the invention for screening drug candidates. The method comprises adding a drug candidate to a cell that expresses an expression profile gene correction for screen bloadtive agents for the ability to bind to drug candidate on the expression of the expression profile gene. The new methods are used to screen bloactive agents for the ability to bind to candidate colorectal cancer drug. An antibody to CGA7 or CJA8 can inhibit the activity of CGA7 or CJA8, respectively, and is used to screen for an agent that can interfere with the binding of CGA7 or CJA8 to the activity of CGA7 or CJA8, respectively, and is used to screen for an agent that can interfere with the binding of CGA7 or CJA8 to the activity of CGA7 or CJA8 is used to inhibit colorectal cancer tissue, where the therapeutic group is a cytotoxic agent or a radioisotope. Antisense molecules are used to inhibit colorectal cancer in a cell. Nucleic acid segments encoding CGA7 or CJA8 are used to alicit an immune response. CGA7 or CJA8 is used to clorectal cancer.

Nucleic acid encoding CGA7 or CJA8 can be used to water the prognosis of an individual with colorectal cancer.
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Disclosure; Fig 8; 40pp; English
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FSACFDNFTEALAETACROMGYSSKPTFRAVEIGPDODLDVVEITENSQELRMRNSSGPC
                                                                                                                     AHCFRKHTDVFNWKVRAGSDKLGSFPSLAVAKIIIIEFNPMYPKDNDIALMKLQFPLTFS
                                                                                                                                                                                                  GTVRPICLPFFDEELTPATPLWIIGWGFTKONGGKMSDILLOASVOVIDSTRCNADDAYO
                                       LSGSLVSLHCLACGKSLKTPRVVGGEEASVDSWPWQVSIQYDKQHVCGGSILDPHWVLTA
                                                             GEVTEXMMCAGIPEGGVDTCQGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein; 437
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21-MAY-2001; 2001US-292544P.
08-AUG-2001; 2001US-310801P.
01-OCT-2001; 2001US-326370P.
04-DEC-2001; 2001US-336780P.
20-FEB-2002; 2002US-358985P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          kinases, phosphatases, proteases, transporters, receptors or transcription factors), useful for colon cancer, gastric cancer, sarcoma, lymphoma
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ve 0; Mismatches 0
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                                               Translational profiling;
phosphatase; protease; pr
cytoskeletal protein; rec
major histocompatability
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              Human expressed protein
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21-MAY-2001; 2001US-2925
08-AUG-2001; 2001US-3108
01-OCT-2001; 2001US-3263
04-DEC-2001; 2001US-3367
20-FEB-2002; 2002US-3569
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                                                                                                                                    gastric cancer; adenoca
leukaemia.
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polypeptide. The purified polypeptide, or the antibody that binds to this polypeptide, is useful for treating cancer. The polypeptide is also useful for identifying compounds that binds to a naturally processed class I or class II MHC-binding polypeptide. The polypeptides and polynucleotides are particularly useful for treating or preventing myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma, lymphoma or leukaemia. These are also useful for screening agents for treating the above mentioned diseases. This sequence represents an expressed protein tag (BPT) isolated from human tissue for translational profiling.
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protease inhibitor; transporter;
receptor; transcription factor; cancer;
ty complex; myeloma; colon cancer;
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100.0%; Pred. No. 9e-
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The invention describes a purified polypeptide, which comprises a fragment of a kinase, phosphatase, protease, protease inhibitor, correspondent of transporter, cytoskeletal protein, receptor or transcription factor.

CC transporter, cytoskeletal protein, receptor or transcription factor.

The polypeptide is useful as an immunogenic composition for eliciting in a mammal an immunogenic response directed against any of the purified polypeptide. The purified polypeptide, or the antibody that binds to this polypeptide, is useful for treating cancer. The polypeptide is also useful for treating compounds that binds to a naturally processed class I or class II MHC-binding polypeptide. The polypeptides and polynucleotides are particularly useful for treating or preventing myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma, clymphoma or leukaemia. These are also useful for screening agents for treating the above mentioned diseases. This sequence represents an priling.

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tion factors), useful for
nucer, sarcoma, lymphoma
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100.0%; Pred. No. 9e-194;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 2; SEQ ID No 1601; 134pp; English
                                                                                                                                                                                                                                                                                                                           Urban
                                                28-MAR-2001; 2001US-279495P.
21-MAY-2001; 2001US-292544P.
08-AUG-2001; 2001US-310801P.
01-OCT-2001; 2001US-326370P.
04-DEC-2001; 2001US-336780P.
20-FBB-2002; 2002US-358985P.
2002WO-US09671
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WO200278524-A2 Homo sapiens,

leukaemia.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention describes a purified polypeptide, which comprises a fragment of a kinase, phosphatase, protease inhibitor, transporter, cytoskeletal protein, receptor or transcription factor.

The polypeptide is useful as an immunogenic composition for eliciting in a mammal an immunogenic response directed against any of the purified polypeptide, or the antibody that binds to this polypeptide, is useful for treating cancer. The polypeptide is also useful for identifying compounds that binds to a naturally processed class I or class II MHC-binding polypeptide. The polypeptides and polynucleotides are particularly useful for treating or preventing myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma, lymphoma or leukaemia. These are also useful for screening agents for treating the above mentioned diseases. This sequence represents an expressed protein tag (EPT) isolated from human tissue for translational
   421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Note: This sequence does not appear in the printed specification but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   kinases, phosphatases, proteases, transporters, receptors or transcription factors), useful for colon cancer, gastric cancer, sarcoma, lymphoma
               364 GEVTEKYMCAGIPEGGVDTCQGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVS
                                                                                                                                                                                                                                                        MHC;
                                                                                                                                                                                                                           Translational profiling; expressed protein tag; EPT; kinase; phosphatase; protease inhibitor; transporter; cytoskeletal protein; receptor; transcription factor; cancer; major histocompatability complex; myeloma; colon cancer; gastric cancer; adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
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                                                                                                                                ABU04936 standard; Protein; 437
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2001US-292544P.
2001US-310801P.
2001US-326370P.
2001US-336780P.
                                                                                                                                                                                                      expressed protein tag
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                                              AYLNWIYNVWKAEL 435
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                                                                                                                                                                              (first entry)
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                                                             424 AYLNWIYNVWKAEL
GEVTEKMMCAGIP
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21-MAY-2001,
08-AUG-2001,
01-OCT-2001,
04-DEC-2001,
20-FEB-2002,
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ABU04936
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                                                                                                 DPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPIIIALLSLASIIIVVVLIKVILDKYYFL
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                                                                            DPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPIIIALLSLASIIIVVVLIKVILDKYYFL
                                                                                                                                                          CGOPLHFIPRKOLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNW
                                                                                                                                                                               CGQPLHFIPRKQLCDGELDCPLGEDEEHCVKSPPEGPAVAVRLSKDRSTLQVLDSATGNW
                                                                                                                                                                                                                                                                                                                                                                                                                               244 AHCFRKHTDVFNWKVRAGSDKLGSFPSLAVAKIIIIEFNPMYPKDNDIALMKLQFPLTFS
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                                          Gaps
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                                       ·;
    437;
   Length
                                       Indels
Core 2337; DB 24;
Pred. No. 9e-194;
Mismatches 0;
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                   ilarity 100.0%; E
Conservative 0;
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 98.86;
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N-PSDB; AAD02557.
                   Similarity
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                                    434;
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uthritis, chronic obstructive pulmonary disease, disorders, stroke, angiogenesis and aberrant
                                                                                                                                                                                                                                                                                                                                                                                                                         eripancing gness are useful in chromosome localisation studies, as tools for tissue expression studies also in gene therapy. The polypeptides of the invention are used for identifying agonists and antagonists useful for treating conditions associated with seripancin imbalance. These polypeptides are also useful as vaccines. The present sequence is seripancin variant #1 protein. The seripancin gene is located on human chromosome 11q22-q23.
                                                                                                                                                                                    polypeptides encoded by them. Seripancian polynucieculass, and protease family. This protein contains a transmembrane domain, a low density lipoprotein (LDL) domain, protease domain and a scavenger receptor cysteine-rich (SRCR) domain. The LDL and SRCR domains help to define the specificity of seripancial's intra and intermolecular interactions. The polynucleotides and polypeptides of the invention are useful for treating and diagnosing diseases such as arthritis, chronic obstructive pulmonary disorder (COPD), cancer, osteoporosis, aberrant wound healing, angiogenesis, inflammatory disorders, diabetes, stroke and cardiovascular diseases. Seripancin genes are useful in chromosome localisation studies,
   Seripancrin, useful for treating
                                                                                                                                                                       relates to seripancrin polynucleotides,
                                                                                                                           English
       ne protease
                                                                                                                             45pp;
                                                                                                                         43-44;
                           cancer, osteoporosis, ediabetes, inflammatory wound healing
                                                                                                                                                                     The present invention
extracellular
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492 AA; Sequence

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                                                        /KPLRKPRIPMETFRKVGIPIIIALLSLASIIIVVVLIKVILDKYYF
                                                                                                      CDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGN
                                                                                                                          LCGQPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGN
                                                                                                                                                                            AETACROMGYSSKPTFRAVEIGPDODLDVVEITENSOELRMRNSSGP
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                                                                              VKPLRKPRIPMETFRKVGIPIIIALLSLASIIIVVVLIKVILDKYYF
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                                    Gaps
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       Score 2329; DB 22; Length 492;
Pred. No. 5.1e-193;
); Mismatches 0; Indels 0
                                                                                                                                                     AETACROMGYSSKPTFRAVEI
99.4%; SUL
100.0%; Pre
    Query Match
Best Local Similarity 100.
Matches 432; Conservative
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                                                       MDPDSDQPLNSLD
                                                                       MDPDSDQPLNSLD
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                                                                                                     LCGOPLHFIPRKO
                                                                                                                                                                                                     CLSGSLVSLHCLA
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The invention describes a purified polypeptide, which comprises a fragment of a kinase, phosphatase, protease, protease inhibitor, transporter, cytoskeletal protein, receptor or transcription factor. The polypeptide is useful as an immunogenic composition for eliciting in a mammal an immunogenic response directed against any of the purified polypeptide, or the antibody that binds to this polypeptide. The purified polypeptide, or the antibody that binds to this polypeptide, is useful for treating cancer. The polypeptide is also useful for identifying compounds that binds to a naturally processed class I or class II MHC-binding polypeptide. The polypeptides are particularly useful for treating or preventing myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma, lymphoma or leukaemia. These are also useful for screening agents for treating the above mentioned diseases. This sequence represents an expressed protein tag (BPT) isolated from human tissue for translational profiling.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       specification but was
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                                                                            MHC;
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                                                     phosphatase; protease; protease inhibitor; transporter; cytoskeletal protein; receptor; transcription factor; cancer; major histocompatability complex; myeloma; colon cancer; gastric cancer; adenocarcinoma; sarcoma; melanoma; lymphoma;
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                                      kinase;
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                                    Translational profiling; expressed protein tag; EPT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Note: This sequence does not appear in the printed obtained in electronic format directly from WIPO at Itp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99.4%; Score 2329; DB 24;
100.0%; Pred. No. 5.1e-193;
ive 0; Mismatches 0;
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 protein tag (EPT)
                                                                                                                                                                                                                                                                                                          28-MAR-2001; 2001US-279495P.
21-MAY-2001; 2001US-292544P.
08-AUG-2001; 2001US-310801P.
01-OCT-2001; 2001US-326370P.
04-DEC-2001; 2001US-336780P.
20-FEB-2002; 2002US-358985P.
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                                                                                                                                                                 Homo sapiens.
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RESULT 13 ABU04913 ID ABU04

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          kinases, phosphatases, proteases, transporters, receptors or transcription factors), useful for colon cancer, gastric cancer, sarcoma, lymphoma
                                         3BLTPATPLWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAY
                                                                                                                                EGGVDTCQGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKV
                                                                                                                                             CGKSLKTPRVVGGEEASVDSWPWQVSIQYDKQHVCGGSILDPHWVLT
                                                                                                 3ELTPATPLWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAY
                                                                                                                                                                                                                                                                                                                                           y; expressed protein tag; EPT; kinase; protease inhibitor; transporter; receptor; transcription factor; cancer; ty complex; myeloma; colon cancer; arcinoma; sarcoma; melanoma; lymphoma;
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2001US-292544P.
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                                                                                                                                                                                                                                                                                                                                           profiling;
                                                                                                                                                                                                                                                                                                                                                     phosphatase; protease; proytoskeletal protein; remajor histocompatability gastric cancer; adenocareleukaemia.
                                                                                                                                                                                                                                                                                                                        Human expressed protein
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CLSGSLVSLHCLAC
                  cissivsincia
                                                       AAHCFRKHTDVFN
                                                                                                 SGTVRPICLPFFD
                                                                                                                                OGEVTERMMCAGI
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                                                                                                                                             QGEVTEKMMCAGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polypeptides (e.g. cytoskeletal proteins, treating cancer, e.g.
                                                                                                                                                                                       SAYLNWIYNVWK
                                                                                                                                                                           SAYLNWIYNVWK
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                                                                                                                                                                                                                                                                                                                                            Translational
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21-MAY-2001;
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this polypeptide, is useful for treating cancer. The polypeptide is also useful for identifying compounds that binds to a naturally processed class I or class II MHC-binding polypeptide. The polypeptides and polynucleotides are particularly useful for treating or preventing myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma, lymphoma or leukaemia. These are also useful for screening agents for treating the above mentioned diseases. This sequence represents an expressed protein tag (EPT) isolated from human tissue for translational profiling.
                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                              Note: This sequence does not appear in the printed specification but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                MDPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPIIIALLSLASIIIVVVLIKVILDKYYF
                                                                                                                                                                                                                                                                                                                                                                           LCGQPLHFIPRKQLCDGBLDCPLGEDEBHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLSGSLVSLHCLACGKSLKTPRVVGGEBASVDSWPWQVSIQYDKQHVCGGSILDPHWVLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAHCFRKHTDVFNWKVRAGSDKLGSFPSLAVAKIIIIEFNPMYPKDNDIALMKLQFPLTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAHCERKATDVFNWKVRAGSDKLGSFPSLAVAKIIIIEPNPMYPKDNDIALMKLOFPLTF
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                                                                                                                                                                                                                                                                                                                                                                                                                                           WFSACFDNFTEALAETACROMGYSSKPTFRAVEIGPDODLDVVEITENSOELRMRNSSGP
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                                                                                                                                                                                                                                                 Length
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100.0%; Pred. No. 5.1e-193;
:ive 0; Mismatches 0;
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205..437
/label= Protease_doms
204..205
310
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Best Local Similarity 100.
Matches 432; Conservative
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                                                                                                                                                                                                                 492 AA;
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Misc-difference
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Novel single chain polypeptide comprising protease domain of type-II membrane-type serine protease or its catalytically active portion useful for treating and preventing cancer and tumor
"Unpaired cysteine
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                                          03471
                                                        79982
83542
                                                       2000US-017
2000US-018
2000US-021
2000US-022
2000US-065
  /note=
                                          2001WO-US
                                                                                                        (CORV+) CORVAS INT INC
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                                                                                                                     Ong EO,
                                                                                                                                  WPI; 2001-488877/53.
                                                                                                                                         N-PSDB; AAD13114
              WO200157194-A2
                                                       03-FEB-2000;
18-FEB-2000;
22-JUN-2000;
26-JUL-2000;
08-SEP-2000;
22-SEP-2000;
                                          02-FEB-2001;
                                                                                                                    Madison EL,
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The invention relates to transmembrane serine proteases and their corresponding nucleotides and the protease domain of a type-II membrane-type serine protease (MTSP). MTSP is useful for identifying compounds that modulate or inhibits its proteolytic activity and for formulating a medicament for treating neoplastic disease. MTSP and its corresponding nucleotides are useful in preventing or treating tumours or cancers such as lung carcinoma, colon adenocarcinoma and ovarian carcinoma, in diagnostics and in hybridisation assays. MTSP is useful as a diagnostic marker for tumour development, growth and/or progression and as immunogens to generate antibodies that specifically bind to it. MTSP DNA is useful in a yeast two-hybrid system and in gene therapy. The present sequence is human MTSP3 protein.
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Pred. No. 3.2e-192;
0; Mismatches 2;
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Best Local Similarity 99.5%;
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November 23, 2003,

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Sequence 6, Appli
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28 477 20.4 312 4 US-09-023-942A-4 29 475 20.3 407 4 US-09-734-675-4 30 472.5 20.2 317 4 US-09-386-629-7 31 467.5 20.0 290 4 US-09-644-600-10 32 467.5 20.0 290 4 US-09-644-600-10 34 465.5 19.9 405 4 US-09-734-675-2 34 465.5 19.9 250 3 US-08-944-483-68 35 463 19.8 855 2 US-09-027-337-2 36 458.5 19.6 790 4 US-09-644-600-2 37 458.5 19.6 790 4 US-09-644-600-2 38 458.5 19.6 790 4 US-09-387-375-9 45 455.5 19.4 812 1 US-08-248-629A-1 45 455.5 19.4 812 1 US-08-451-932-1 44 455.5 19.4 812 1 US-08-452-260-1 45 455.5 19.4 812 2 US-08-612-788-1 45 455.5 19.4 812 2 US-08-655-98B-1 45 455.5 19.4 812 2 US-08-655-98B-1	ALIGNMENTS RESHL.T 1	S-09-008-271A-6 Sequence 6, Application US/09008 Patent No. 6203979 GENERAL INFORMATION: APPLICANT: Bandman, Olga Hillman, Jenniy Yue, Henry Guegler, Karl Corley, Neil Corley, Purvi TITLE OF INVENTION: HUMAN NUMBER OF SEQUENCES: 24 CORRESPONDENCE ADDRESS:	STREET: 3174 Porter Dr.  CITY: Palo Alto STATE: CA COUNTRY: USA ZIP: 94304  COMPUTER READABLE FORM: MEDIUM TYPE: Diskette COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/008,271A FILING DATE: 16-Jan-1998  PRIOR APPLICATION DATA: HIGH DATE: CINKNOWN> FILING DATE: CINKNOWN>	ATTORNEY/AGENT INFORMATION:  NAME: Mohan-Peterson, Sheela REGISTRATION NUMBER: 41,201 REFERENCE/DOCKET NUMBER: PF-0458 US TELEPHONE: 650-855-0555 TELEPHONE: 650-845-4166 TELEFAX: 650-855-0555 TELEFAX: 650-855-055 TELEFAX: 650-855 TELEFAX: 650-85

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US-09-342-749-2
; Sequence 2, Application US/09342749
; Patent No. 6166194
; GENERAL INFORMATION:
; APPLICANT: Wong, Alexander K.C.
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Teng, David H.-F.
; TITLE OF INVENTION: TMPRSS2 is a Tumor Suppressor; TITLE OF INVENTION: TMPRSS2 is a Tumor Suppressor; TITLE REFERENCE: 2318-202
; CURRENT APPLICATION NUMBER: US/09/342,749
; CURRENT FILING DATE: 1999-06-29
; BARLIER FILING DATE: 1998-06-29
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.0
; TYPE: PRI
; TYPE:
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US-09-342-749-2
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Pred. No. 6.2e-231;
1; Mismatches 0;
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Patent No. 645568

GENERAL INFORMATION:
APPLICANT: Mack, David
APPLICANT: Gish, Kurt
APPLICANT: Wilson, Keith
TITLE OF INVENTION: NOVEL METHODS OF DIAGNOS
TITLE OF INVENTION: OF SCREENING FOR COLORE;
FILE REFERENCE: A-69108/DJB/JJD/AMS
CURRENT FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: US 09/525,993
PRIOR FILING DATE: 2000-03-15
PRIOR FILING DATE: 2000-01-28
PRIOR FILING DATE: 2000-01-28
PRIOR FILING DATE: 2000-01-28
PRIOR FILING DATE: 2000-03-15
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                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Wong, Alexander K.C.

APPLICANT: Tavtigian, Sean V.

APPLICANT: Tavtigian, Sean V.

APPLICANT: Tavtigian, Sean V.

APPLICANT: Tavtigian, Sean V.

TITLE OF INVENTION: TMPRSS2 is a Tumor Suppressor

FILE REFERENCE: 2318-202

CURRENT APPLICATION NUMBER: US/09/691,840

CURRENT FILING DATE: 2000-10-18

PRIOR APPLICATION NUMBER: US/09/342,749

PRIOR FILING DATE: 1999-06-29

PRIOR FILING DATE: 1998-06-29

NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patentin Ver. 2.0
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TDWIYRQMRAD 491
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US-09-518-046-2
Sequence 2, Application US/09518046
Patent No. 6294663
GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
APPLICANT: Underwood, Lowell J.
                                                                                                                              |||| | : :||| | :||
468 AYRPGVYGNVMVFTDWIYRQMRAD
                                                                                            PSTPGVYTKVSAYLNWIYNVWKAE
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NRCVRLY--GP.
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Patent No. 6444419
GENERAL INFORMATION:
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Best Local Similarity 3:
Matches 150; Conservati
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ORGANISM: Homo sapiens
-09-691-840-2
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LENGTH: 492
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PROTEINS, ENCODING HUMAN PROTEASE PROTEINS,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44 LPPBVFSQSSLGIIAL----ILALAIGLGIHFDCSGKYRCRSFKC---IELITR---
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TITLE OF INVENTION: Transmembrane Serine Protease Overexpressed

TITLE OF INVENTION: in Ovarian Carcinoma and Uses Thereof
FILE REFERENCE: D6192CIP
CURRENT APPLICATION NUMBER: US/09/518,046
CURRENT FILING DATE: 2000-03-02
FARLIER APPLICATION NUMBER: 09/261,416
FARLIER PILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 153
SEQ ID NO 2
IENGTH: 454
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE: ORGANISM: TOWNER OF TRANSMEMBRE OF SAPING OF TRANSMEMBRE OF TRANSMEMBRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 IPMETFRKVGIPILIALLSLASIIIVVVLIKVILD---KY
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Patent No. 6482630;
GENERAL INFORMATION:
APPLICANT: Gan, Weiniu
APPLICANT: Ye, Jane
APPLICANT: DiFrancesco, Valentina
APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROFUNCE INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
TITLE TO INVENTION: USES THEREOF
TITLE REFERENCE: CL001194
CURRENT FILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 417
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RAGSDKLGSFPSLAVAKIIIIEFNPMYP----
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|CADVNKPGVYTRVTSFLDWIHEOMERDL
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                                                 ETACROMGYSS-
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ORGANISM: HUMAN
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LENGTH: 376
TYPE: PRT
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                                                                                                                                                                                                                       ---SQELRMRNSSGPCLS 183
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                                                                                                                                                                                             90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Squence 12. Application US/09261416A
Patent No. 6291663
GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
APPLICANT: Underwood, Lowell J.
ITILE OF INVENTION: TADG-12: A No. 6291663el Transmembrane Serine Protease
TITLE OF INVENTION: Overexpressed in Ovarian Carcinoma
FILE REFERENCE: D6192
CURRENT APPLICATION NUMBER: US/09/261,416A
CURRENT FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleotides
                                                                                                                                                              79 LDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNWFSACFDNFTEALAETAC
                                                                                                                                                                                                                                                                                                                                                                             LOFPLIFSGTVRPICLPFFDEELTPATPLWIIGWGFTKONGGKMSDILLQASVOVIDSTR
                                                                                                                                                                                                                                                                                                                                                                                                                                 CNADDAYQGEVTEKMMCAGIPEGGVDTCQGDSGGPLMYQ----SDQWHVVGIVSWGYGC
                                                                                                         19 KPRIPMETFRKVGIPIIIALLSLASIIIVVVLIKVILDKYYFLCGQPLHFIPRKQLCDGE
                                                                                                                                                                               BEMGF-----LRAL---THSELDVRTAGANGTSGFFCVDEGRLPHTQRLLEVISPSDCPR
                                                                                                                                                                                                                                                                    184 GSLVSLHCLACG-KSLKTPRVVGGEEASVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAA
                                                                                                                                                                                                                                                                                        CNGADFYGNOIKPKMFCAGYPEGGIDACQGDSGGPFVCEDSISRIPRWRLCGIVSWGTGC
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                                                            Length 417;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24.9%; Score 584; DB 3; Length 45. larity 34.2%; Pred. No. 3.2e-51; Conservative 73; Mismatches 150; Indels
                                                                                                                                                                                                                                                                                                                           HCFRKHTDVFN-WKVRAGSDKLGSFPSLAVAKIIIIEFNPMYP
                                                       25.1%; Score 588.5; DB 4;
31.5%; Pred. No. 9.7e-52;
ive 60; Mismatches 161;
                                                                                                                            :|:: | | | | ||::
15 RPKVAALT---AGTLLLLTAIGAASWAIVAVLLR
                                                                                                                                                                                                                   139 ROMGYSSKPTFRAVEIGPDODLDVVEITEN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  o acid sequence of 1
to 1511 of Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    382 ALAQKPGVYTKVSDFREWIFQAIK 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     409 GGPSTPGVYTKVSAYLNWIYNVWK 432
                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
CTHER INFORMATION: Amino
CTHER INFORMATION: 144 tc
Patent No. 6291663
US-09-261-416-2
                                                                                                                                                                                        ----SDOE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
                                                      Query Match
Best Local Similarity
Matches 140; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 153; Conser
; TYPE: PRT
; ORGANISM: HUMAN
US-09-820-002-4
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SEQ ID NO 2
" THYTH: 455
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US-09-261-416-2
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||: : || : | : | : | : | ----VRVGGQNAVLQVFTAA--SWKTMCSDDWKGHYA
                                                                                                                                                                                                                                                     AHCFRKHTDVF---NWKVRAGSDKL--GSPPSLAVAKIIIIEFNPMY-PK--DNDIALMK
                                                                                                                                                                                    LQFPLTFSGTVRPICLPFFDEELTPATPLWIIGWGFTKQNGGKMSDILLQASVQVIDSTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---KPTFRAVEIGPDQDLDVVEITENSQELRMRNSSGPCL
                                                                                                     SGSLVSLHCLACG-KSLKTPRVVGGBEASVDSWPWQVSIQYDKQHVCGGSILDPHWVLTA
                                                                                                                                                                                                                                                                                                 AHCV---YDLYLPKSWTIQVGLVSLLDNPAPSHLVEKIV---YHSKYKPKRLGNDIALMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CNADDAYQGEVTEKMM----CAGIPEG-GVDTCQGDSGGPLMYQSDQ-WHVVGIVSWGYG
                                                                                                                                                                                                                                                                                                                                                                                 311 LAGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGAT-EDGGDASPVINHAAVPLIS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LDCPLGEDBEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNWFSACFDNFTEALAETAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KPRIPMETERKVGIPIIIALLSLASIIIVVVLIKVILDKYYFLCGQPLHFIPRKQLCDGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                139 ROMGYSSKPTFRAVEIGPDQDLDVVEITENSQELRMRNSSGPCLSGSLVSLHCLACG-KS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --PLYPVQVSSADARLMVFDKTEGTWRLLCSSRSNARVAGLSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----DCPRGRFLAAICQDCGRRK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LPVDRIVGGRDTSLGRWPWQVSLRYDGAHLCGGSLLSGDWVLTAAHCFPERNRVLSRWRV
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ENCODING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 30.8%; Pred. No. 6.2e-51
Matches 132; Conservative 57; Mismatches 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/09820002; Patent No. 6482630; GENERAL INFORMATION:
; APPLICANT: Gan, Weiniu
; APPLICANT: Ye, Jane
; APPLICANT: DiFrancesco, Valentina
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PRC;
; TITLE OF INVENTION: USCLATED HUMAN PROTEASE PRC;
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001194
; CURRENT APPLICATION NUMBER: US/09/820,002
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FRESESC FOR WINGOWS VERSION 4.0
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--CPRGRFLTA 147
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                                                                                                                            TCQDCGRRKLPVDRIVGGQDSSLGRWPWQVSLRYDGTHLCGGSLLSGDWVLTAAHCFPER
                                                                                                                                                                         300 FSGTVRPICLPFFDEELTPATPLWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDA
                                                                                                                                                                                                249 IDVFN-WKVRAGSDKLGSFPSLAVAKIIIIEFNPMYP-----KDNDIALMKLQFPLT
                                                                                                                                                                                                                                           YQGEVTEKMMCAGIPEGGVDTCQGDSGGPLMYQ----SDQWHVVGIVSWGYGCGGPSTP
                                                                                                                                                                                                                                                                  69 IPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNWFSACFDN
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; Pred. No. 1.6e-49;
67; Mismatches 138;
      101 SELDVRTAGANGTSGFFCVDEGGLRLAQRLLDVISVCD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
TITLE OF INVENTION: CLONING OF ENTEROKIN
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc. -
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: MA
COUNTRY: USA
ZIP: 02140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLUE.

COMPUTER: IBM PC COMPALLL.

COMPUTER: Patentin Release #1.0, Vers:
SOFTWARE: Patentin Release #1.0, Vers:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/200,900A
FILING DATE: 23-FEB-1994
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: Meinert, Maureen C.
REGISTRATION NUMBER: 31,544
REFERENCE/DOCKET NUMBER: GI 5201-FWC
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170 X8574
TELEPHONE: (617) 876-5851
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
TENGTH: 798 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/08200900A
Patent No. 5665566
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                              GVYTKVSAYLNWIYNVWK 432
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GVYTKVTDFREWIFKAIK 404
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35.0%;
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Matches 133; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                        148
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 QLGVQAVVYHGGYLPFRDPNSEENSNDIALVHLSSPLPLTEYIQPVC 236
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                                                        QGDSGGPLMYQ----SDQWHVVGIVSWGYGCGGPSTPGVYTKVSAY
                                                                                                                         CVKSFPEGPAVAVRLSKDRSTLQVLDSATGNWFSACFDNFTEALAETACRQMGY-----
                                     LPFFDEELTPATPLWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :IIIVVVLIKVILDKYYFLCGQPLHFIPRKQLCDGELDCPLGEDEEH
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                                                                                                                                                                                                                                                                                                                                                                               OCKOUT MICE AND THEIR PROGENY SRUPTED SERINE PROTEASE GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/866,058
FILING DATE: 30-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: LEBOVITZ, RICHARD M.
REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: BERLX 65P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEPACE: 703-243-6410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24.5%; Score 574; 30.8%; Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                              WHITE, ZELANO & IDON BLVD. SUITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US/09/000,846
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C-DOS/MS-DOS
Release #1.0,
                                                                                                                                                                                                                                           RESULT 9
US-09-000-846-2
Sequence 2, Application US/09000846
Patent No. 5981830
GENERAL INFORMATION:
APPLICANT: WU, QINGYU
APPLICANT: SADLER, JASPER
ITLE OF INVENTION: KNOCKOUT MICE
ITLE OF INVENTION: DISRUPTED SEF
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELA
STREET: 2200 CLARENDON BLVD. 5
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VGTLLFLTGIGAÁSWAİVTIĹLQ
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Z2201
ZOMPUTER READABLE FORM:
MEDIUM TYPE: Floppy d
COMPUTER: IBM PC comp
OPERATING SYSTEM: PC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 703-22 INFORMATION FOR SEQ ID NO SHOUENCE CHARACTERISTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin R
CURRENT APPLICATION DAT
APPLICATION NUMBER:
FILING DATE: 30-DEC-
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amino acid
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                                                                                                    369 MCAGIPEGGVDTC
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177 FAGAVAQASPHGL
                                                                                                                                                                        424 LNWIYNVWK
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; MOLECULE TYPE:
US-09-000-846-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             135;
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                                                                                                                                     296
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Best Local S
Matches 135
                                      309
                                                                   237
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FOR PRODUCING THE ENZYME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72
 ----GEDEEHCVKSFPEG-----PAVAVRLSKD----RSTLQVLDSATGNWFSACFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          186 LVSLHCLACGKSLKTPRVVGGEEASVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YRTLSGRIESLITKTFKESNLRNQFIRAHVAKLRQDGSGVRADVVMKFQFTRNNNGASM-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     128 NFTEALABTACROMGYSSKPTFRAVEIGPDQDLDVVEITENSQELRMRN--SSGPCLSGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----TLSEORILGGTEAEEGSWPWQVSLRLNNAHHCGGSLINNWWILTAAHCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIIIALLSLASIIIVVVLIKVILDKYYFLCGQPLHFIPRK--QLCDGELDCPI
                                                                                                                                                                                                                                                                        ENCODING
ID PROCESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 24.3%; Score 568; DB 1; L. Best Local Similarity 32.4%; Pred. No. 1.2e-49; Matches 138; Conservative 79; Mismatches 149;
                                                                                                                                                                                                                                            TITLE OF INVENTION: NUCLEIC ACID SEQUENCE ENTITLE OF INVENTION: TRYPSIN-LIKE ENZYME AND NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack STREBT: 805 Fifteenth Street, N.W., #700 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                뒫
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         July 28, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.5 inch,
                                                                                                                                                                        US-08-508-448C-25
; Sequence 25, Application US/08508448C
; Patent No. 5804410
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTR:
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5
THE COMPATION TYPE: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
                                                                                CALPNRPGVYARVPRFTEWI
                                                             CGGPSTPGVYTKVSAYLNWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                               CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
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US-08-508-448C-25
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                                                                                                                                                                                                                                                              349 IDSTRCNADDAYQGEVTERMMCAGIPEGGVDTCQGDSGGPLMYQ-SDQWHVVGIVSWGYG
                                                                                                                                                                                                             CLSGSLVSLHC--LACGKSLKT----PRVVGGEBASVDSWPWQVSIQYDKQHVCGGSILD
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                                       LACGKSLKT----PRVVGGEEASVDSWPWQVSIQYDKQHVCGGSILD
                                                            596 RDWLVSAAHCVYGRNMEPSKWKAVLGLHMASNLTSPQIETRLIDQIVINPHYNKRRKNND
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486 WITQISDDVCQLLGLGTGNSSVPTF-STGGGPYVNLNTAPNGSLILTPSQQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL TAPPLICANT:

TITLE OF INVENTION: CLONING
NUMBER OF SEQUENCES: 33
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

TOMPUTER: IBM PC compatible

TOMPUTER: IBM PC compatible

TOMPUTER: IPM PC compatible

TOMPUTER: IPM PC compatible

TOMPUTER: IPM PC compatible

TOMPUTER: IPM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, V CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/00616 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCT-US94-00616-2; Sequence 2, Application PC/TUS9400616; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                         CGGPSTPGVYTKVSAYLNWI 427
                                                                                                                                                                                                                                                                                                                                                               CALPNRPGVYARVPRFTEWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 3:
Matches 133; Conservati
                                      CLSGSLVSLHC-
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Query Match

24.3%; Score 568; DB 4; L

Best Local Similarity 32.4%; Pred. No. 1.2e-49;

Matches 138; Conservative 79; Mismatches 149;
                                                                                                                                                          Sequence 83, Application US/09370838 Patent No. 6444425 GENERAL INFORMATION:
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Patent No. 6444425
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Mohamath, Roadoh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Homo sapien
US-09-370-838-83
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407 AYLDWI 412
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US-09-370-838-62
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US-09-370-838-82

Sequence 82, Application US/09370838

Patent No. 6444425

GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Mohamath, Roadoh
APPLICANT: Mohamath, Roadoh
TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF
TITLE OF INVENTION: LUNG CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.475C1
CURRENT APPLICATION NUMBER: US/09/370,838
CURRENT FILING DATE: 1999-04-02
NUMBER OF SEQ ID NOS: 289
SOFTWARE: FASLSEQ for Windows Version 3.0
SEQ ID NO 82
LENGTH: 418

TYPE: PRT
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JS-09-370-838-82
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Best Local Similarity
Matches 138; Conser
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AYLDWI
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APPLICANT: Reed, Steven G.

APPLICANT: Lodes, Michael J.

APPLICANT: Lodes, Michael J.

APPLICANT: Lodes, Michael J.

APPLICANT: Lodes, Michael J.

APPLICANT: Mohamath, Roadoh

APPLICANT: Secrist, Heather

TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF

TITLE OF INVENTION: LUNG CANCER AND METHODS FOR THEIR USE

FILE REFERENCE: 210121.475C1

CURRENT APPLICATION NUMBER: US/09/370,838

CURRENT APPLICATION NUMBER: US 09/285,323

EARLIER APPLICATION NUMBER: US 09/285,323

EARLIER PILING DATE: 1999-04-02

NUMBER OF SEQ ID NOS: 289

SOFTWARE: FastSEQ for Windows Version 3.0
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APPLICANT: Secrist, Heather

TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF

TITLE OF INVENTION: LUNG CANCER AND METHODS FOR THEIR USE

TITLE OF INVENTION: LUNG CANCER AND METHODS FOR THEIR USE

CURRENT APPLICATION NUMBER: US/09/370,838

CURRENT FILING DATE: 1999-08-09

BARLIER APPLICATION NUMBER: US 09/285,323

BARLIER FILING DATE: 1999-04-02

NUMBER OF SEQ ID NOS: 289

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 62

LENGTH: 418

TYPE: PRT

ORGANISM: Homo sapien

US-09-370-838-62
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; Pred. No. 2e-49;
80; Mismatches 149; Indels
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Best Local Similarity 32.2%
Matches 137; Conservative
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Job time: 25.1389 secs
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2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
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version 5.1.6
- 2003 Compugen Ltd.
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US-10-015-387A-275

US-10-063-735-112

US-10-06-130A-275

US-10-199-672-330

US-10-187-749-330

US-10-184-642-330

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## ALIGNMENTS

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RESULT 1
US-10-180-719-6

| US-10-180-719-6
| Sequence 6, Application US/10180719
| Publication No. US20030166246A1
| GENERAL INFORMATION:
| Hallman, Jennifer L. Yue, Henry Guegler, Karl J. Corley, Neil C. Tang, Tow Y. Shah, Purvi Shah, Purvi Shah, Purvi Shah, Purvi Shah, Purvi Corley. Neil C. STREET: 3174 Porter Dr. CITTLE OF INVENTION: HUMAN PROTEASE MOLECULES NUMBER OF SEQUENCES: 24
| CORRESPONDENCE S. 24
| COUNTY: Palo Alto STREET: 3174 Porter Dr. CITY: Palo Alto STATE: CA COUNTRY: USA ZIPP: 94304 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette COMPUTER READABLE FORM: MEDIUM TYPE: Diskette COMPUTER: IBM Compactable OPERATING SYSTEM: DOS CURRENT APPLICATION NUMBER: US/10/180,719 FILING DATE: 25-Jun-2002 PRIOR APPLICATION NUMBER: US/10/180,711 FILING DATE: 16-Jun-1998 ATTORNEY/AGENT INFORMATION:
| NAME: Mohan-Peterson, Sheela REGISTRATION INFORMATION: TELECOMMUNICATION INFORMATION:
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i Sequence 4, Application US/09776191

j Publication No. US20030119168A1

j GENERAL INFORMATION:

j APPLICANT: Edwin L. Madison

APPLICANT: Edwin L. Madison

APPLICANT: Grass International, Inc.

TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING

TITLE OF INVENTION: NUCLEIC ACID MOLECULES

TITLE OF INVENTION: NUMBER: US/09/776,191

CURRENT APPLICATION NUMBER: 60/213,124

PRIOR FILING DATE: 2000-06-22

PRIOR FILING DATE: 2000-06-22

PRIOR FILING DATE: 2000-06-22

PRIOR FILING DATE: 2000-02-03

PRIOR FILING DATE: 2000-02-03

PRIOR FILING DATE: 2000-02-18

PRIOR FILING DATE: 2000-02-03

PRIOR 
                                                       Score 2337; DB 9; 1 Pred. No. 6.6e-226;
                                      99.8%; Scorred 100.0%; Pred. No. co. o. Mismatches
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Best Local Similarity 100.
Matches 434; Conservative
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Sequence 8, Application US/09851588

Fatent No. US20020042067A1

Fatent No. US20020042067A1

Fatent No. US20020042067A1

Sequence 8, Application US/09851588

PPPLICANT: Mack, David

APPLICANT: Mack, David

APPLICANT: Wilson, Keith E.

TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSING COLORECTAL CANCER, COMITITLE OF INVENTION: OF SCREENING FOR COLORECTAL CANCER MODULATORS

FILE REFERENCE: A-68829-1/DJB/JJD/AMS

CURRENT APPLICATION NUMBER: US/09/851,588

CURRENT FILING DATE: 2001-09-24

PRIOR APPLICATION NUMBER: US 09/656,002

PRIOR APPLICATION NUMBER: US 09/656,002

PRIOR FILING DATE: 2000-09-06

NUMBER OF SEQ ID NOS: 9

SOFTWARE: Patentin version 3.1
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Pred. No. 5.2e-226;
1; Mismatches 0;
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                     INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 435 amino acid
TYPE: amino acid
STRANDEDNESS: single
 845-4166
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IMMEDIATE SOURCE:
LIBRARY: COLNNOT13
CLONE: 1337018
SEQUENCE DESCRIPTION: SEQ
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Best Local Similarity 99.8%;
Matches 434; Conservative
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ORGANISM: Homo sapiens
TELEFAX:
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US-10-180-719-6
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LENGTH: 437
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Pan, James
Paoni, Nicholas F
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ORGANISM: Homo Sapien
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030060612A1

A:
A:A.Adreey
Owski, Paul J.
A:Inlan, Kenneth J.
Smith, Victoria
X: Wood, William I.
ANT: Whod, William I.
ANT: Alang, Zemin

CE INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGN
LE REPREBRICE: P5002R1

ANT: ALANG, Zemin

BRIOR FILING DATE: 1997-10-28

PRIOR FILING DATE: 1998-09-10

PRIOR FILING DATE: 1998-09-10

PRIOR FILING DATE: 1998-10-08

PRIOR FILING DATE: 1998-10-08

PRIOR FILING DATE: 2000-
PRIOR FILING DATE: 1000-F

PRIOR F
    Pred. No. 4.3e-224;
                           Mismatches
                          0
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                             Conservative
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124 FSACFDNFTEALAETACROMGYS-----RAVEIGPDQDLDVVEITENSQELRMRNSSGPC
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Pred. No. 6.1e-222;
0; Mismatches 0; Indels 5;
PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: PCT/US00/23328
PRIOR PILING DATE: 2000-08-24
PRIOR PILING DATE: 2000-12-01
PRIOR PILING DATE: 2000-12-01
PRIOR FILING DATE: 2001-02-28
PRIOR FILING DATE: 2001-02-28
PRIOR FILING DATE: 2001-02-28
PRIOR FILING DATE: 2001-03-01
NUMBER OF SEQ ID NOS: 10
SEQ ID NO 7
LENGTH: 432
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US-09-946-374-275
Sequence 275, Application US/09946374
Publication No. US20030073129A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Godwski, Paul J.
APPLICANT: Godwski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
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Best Local Similarity 98.8%;
Matches 429; Conservative 0
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A APPLICATION NUMBER: 60/100849

RAPPLICATION NUMBER: 60/100849

RAPPLICATION NUMBER: 60/100919

RAPPLICATION NUMBER: 60/100919

RILING DATE: 1998-09-18

RAPPLICATION NUMBER: 60/100919

RAPPLICATION NUMBER: 60/101014

RAPPLICATION NUMBER: 60/101014

RAPPLICATION NUMBER: 60/101014

RAPPLICATION NUMBER: 60/101014

RAPPLICATION NUMBER: 60/101019

RAPPLICATION NUMBER: 60/101071

RAPPLICATION NUMBER: 60/101472

RAPPLICATION NUMBER: 60/101473

RAPPLICATION NUMBER: 60/101916

RAPPLICATION NUMBER: 60/102307

RAPPLICATION NUMBER: 60/102807

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PPLICATION NUMBER: 60/
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APPLICANT: Smith, Victoria APPLICANT: Smith, Victoria APPLICANT: Tumas, Daniel APPLICANT: Tumas, Daniel APPLICANT: Tumas, Daniel APPLICANT: Tumas, Daniel APPLICANT: Walliams, P. Mick APPLICANT: Walliams, P. Mick APPLICANT: Walliams, P. Mick APPLICANT: Wood, Williams, P. Mick APPLICANT: Wood, Williams, P. Mick APPLICANT: Wood, Williams, P. Mick Engles PERRENCE: P283 APPLICANTON NUMBER: 60/PRIOR APPLICATION NUMBER: 60/PRIOR PILING DATE: 1998-09-09/PRIOR APPLICATION NUMBER: 60/PRIOR PILING DATE: 1998-09-09/PRIOR PILING DATE: 1998-09-10/PRIOR P
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US-10-015-387A-275

Sequence 275, Application US/10015387A

Publication No. US20030135034A1

GENERAL INFORMATION:
APPLICANT: Botstein, David
APPLICANT: Battein, David
APPLICANT: Battein, David
APPLICANT: Battein, David
APPLICANT: Ferrara, Napoleone
APPLICANT: Fond, Nerman
APPLICANT: Godowski, Paul J.
APPLICANT: Gotomski, Christopher J.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Paoni, Nicholas F.
TITLE OF INVENTION: Acids Encoding the Same
FILE REPERBUCE: P2830PLCS
TITLE OF INVENTION: Acids Encoding the Same
FILE REPERBUCE: P2830PLCS
TITLE OF INVENTION: Acids Encoding the Same
FILE REPERBUCE: P2830PLCS
CURRENT APPLICATION NUMBER: US/10/015,387A
CURRENT APPLICATION NUMBER: US/10/015,387A
CURRENT APPLICATION NUMBER: US/10/015,387A
SEQ ID NO 275
LENGTH: 432
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Best Local Similarity 98.8%; Pred. No. 6.1e-222;
Matches 429; Conservative 0; Mismatches 0; Indels
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; ORGANISM: Homo sapiens
US-10-015-387A-275
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US-10-063-735-112
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8.8%; Pred. No. 6.1e-222;
ve 0; Mismatches 0; Indels 5;
                                 R: 60/103395
-10-07
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Sequence 112, Application US/10063735

Publication No. US20030138882A1

GENERAL INFORMATION:

APPLICANT: Eaton, Dan L.

APPLICANT: Filvaroff, Ellen

APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Watanabe, Colin K.

APPLICANT: Wood, William I.

TITLE OF INVENTION: ACIDS ENCODING THE SAME

TITLE OF INVENTION: ACIDS ENCODING THE SAME

TITLE OF INVENTION: ACIDS ENCODING THE SAME

TITLE OF INVENTION NUMBER: US/10/063,735

CURRENT FILING DATE: 2002-05-08

Prior Application removed - See Palm or File Wrapper

NUMBER OF SEQ ID NOS: 170

SEC. TH. MONDER:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123
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Pred. No. 6.1e
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0; Mismatches
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APPLICANT: Botstein, David
APPLICANT: Besnoyers, Luc
APPLICANT: Eaton, Dan 1.
APPLICANT: Ferrara, Napoleone
APPLICANT: Forg, Sherman
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Best Local Similarity 98.8%;
Matches 429; Conservative (
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; Sequence 275, Application
; Publication No. US20030146
; GENERAL INFORMATION:
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US-10-063-735-112
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LENGTH: 432
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APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Goddwrd, Paul J.
APPLICANT: Goddwrki, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Pan, 
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APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Chen, Jian
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
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Smith, Victoria
Watanabe, Colin K.
Wood, William I.
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Best Local Similarity
Matches 429; Conser
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; ORGANISM: Homo
US-10-006-130A-275
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             ETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
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Pred. No. 6.1e-222;
0; Mismatches 0; Indels
TITLE OF INVENTION: SECRETED AND TRANSMEMBRAN
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILLE REFERENCE: P3430R1C1
CURRENT APPLICATION NUMBER: US/10/199,672
CURRENT FILING DATE: 2002-07-18
PRIOR PILING DATE: 2002-01-15
PRIOR PILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-0-18
PRIOR PILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063120
PRIOR PILING DATE: 1997-10-24
PRIOR FILING DATE: 1997-10-24
PRIOR PILING DATE: 1997-10-24
PRIOR PILING DATE: 1997-10-24
PRIOR PILING DATE: 1997-10-24
PRIOR PILING DATE: 1997-10-24
PRIOR PRIOR APPLICATION NUMBER: 60/063540
PRIOR FILING DATE: 1997-10-28
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Best Local Similarity 94
Matches 429; Conservati
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ORGANISM: Homo
-10-199-672-330
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RESULT 10 US-10-006-172A-275

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Publication No. 1986-10006172A

Publication No. 1980-10006172A

Publication No. 1980-1000617A

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Tue Nov 25

LSGSLVSLHCLACGKSLKTPRVVGGEBASVDSWPWQVSIQYDKQHVCGGSILDPHWVLTA 4 DPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPIIIALLSLASIIIVVVLIKVILDKYYFL FSACFDNFTEALAETACROMGYS----RAVEIGPDODLDVVEITENSQELRMRNSSGPC DPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPIIIALLSLASIIIVVVLIKVILDKYYFL FSACFDNFTEALAETACROMGYSSKPTFRAVEIGPDQDLDVVEITENSQELRMRNSSGPC Gaps Score 2297.5; DB 12; Length 432; Pred. No. 6.1e-222; 0; Mismatches 0; Indels 5; PRIOR APPLICATION NUMBER: 60/102665
PRIOR APPLICATION NUMBER: 60/10258
PRIOR PILLING DATE: 1998-10-02
PRIOR FILLING DATE: 1998-10-06
PRIOR FILLING DATE: 1998-10-06
PRIOR FILLING DATE: 1998-10-07
PRIOR FILLING DATE: 1998-10-07
PRIOR FILLING DATE: 1998-10-07
PRIOR FILLING DATE: 1998-10-07
PRIOR PILLING DATE: 1998-10-08
PRIOR PILLING DATE: 1998-10-20
PRIOR PILLING DATE: 19 Query Match
Best Local Similarity 98.8%;
Matches 429; Conservative 124 122 182 62 64 a 셤 g  $\delta$ ò

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Sequence 330, Application US/10187749

Publication No. US202030153036A1

Septicant: Baker, Kevin P.

APPLICANT: Baker, Kevin P.

APPLICANT: Chen, Jian

APPLICANT: Godowski, Paul J.

APPLICANT: Mood, William I.

APPLICANT: Mood, William I.

APPLICANT: APPLICANT: Mood, William I.

APPLICANT: APPLICANT: ALISE MOODING THE SAME

TITLE OF INVENTION: ACIDS ENCODING THE SAME

PRICE PRICES 12002-07-01

TITLE OF INVENTION: ACIDS ENCODING THE SAME

PRICE PRICES 12002-07-01

PRICE PRILING DATE: 1997-09-18

PRICE PRILING DATE: 1997-09-18

PRICE APPLICANTION NUMBER: 60/063266

PRICE APPLICANTION NUMBER: 60/063266

PRICE APPLICANTION NUMBER: 60/063240

PRICE APPLICANTION NUMBER: 60/063341

PRICE PRILING DATE: 1997-10-24

PRICE PLILING DATE: 1997-10-28

PRICE PRILING DATE: 1997-10-28

PRICE PLILING DATE: 1997-10-28

PRICE PRICE APPLICANTION NUMBER: 60/063544

PRICE PRILING DATE: 1997-10-28

PRICE PLILING DATE: 1997-10-28

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179 LSGSLVSLHCLACGKSLKTPRVVGGEEASVDSWPWQVSIQYDKQHVCGGSILDPHWVLTA 238
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Pred. No. 6.1e-222;
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98.8%;
                                                                                                                                                                                                                                                                                                                                                               AYLNWIYNVWKAEL 435
                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
CORGANISM: Homo Sapien
US-10-187-749-330
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US-10-187-749-330
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0; Mismatches

Conservative

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APPLICANT: CLEAN, JULEA
APPLICANT: CARACHANTER
APPLICANT: GOGDARA, ANGREY
APPLICANT: GOGDARA, ANGREY
APPLICANT: GOGDARA, ANGREY
APPLICANT: GOGDARA, ANGREY
APPLICANT: GORDARA, PAUSTIN L.
APPLICANT: SAILA, VICTOR
APPLICANT: SAILA, VICTOR
APPLICANT: SAILA, VICTOR
APPLICANT: SAILA, VICTOR
APPLICANT: ARTHORY SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
APPLICANT: MOOD, WIlliam I.
APPLICANT: MOOD, WILLIAM I.
APPLICANT: MOOD SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACCORDER: 10/05286
FILE REFERENCE: P4330R1C26
CURRENT APPLICATION NUMBER: 10/05286
PRIOR PILING DATE: 2002-01-18
PRIOR PILING DATE: 1997-00-18
PRIOR PILING DATE: 1997-00-18
PRIOR PELING DATE: 1997-10-24
PRIOR PELING DATE: 1997-10-24
PRIOR PILING DATE: 1997-10-24
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PRIOR PELING DATE: 1997-10-24
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PRIOR PILING DATE: 1997-10-28
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                                                                                                                                                 Score 2297.5; DB 12; Length
Pred. No. 6.1e-222;
0; Mismatches 0; Indels
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     Wrapper
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APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Chen, Jian
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Austin L.
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Angranabe, Colin K.
APPLICANT: Angranabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Angranabe, Colin K.
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    File
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ER: US/10/184,642
     See
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98.8%;
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Best Local Similarity 98.8
Matches 429; Conservative
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Prior Application data ru
NUMBER OF SEQ ID NOS: 61.
SEQ ID NO 330
LENGTH: 432
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                                                                       TYPE: PRT
ORGANISM: Homo Sapien
US-10-194-457-330
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US-10-184-642-330
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                                                       Gaps
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     Score 2297.5; DB 12; Lengt
Pred. No. 6.1e-222;
0; Mismatches 0; Indels
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Pred. No. 6.1e-222;
0; Mismatches 0;
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APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Mood, William I.
APPLICANT: Thang, Zemin I.
APPLICANT: ApplicaNTON: SECRETED AND TRANSMEMBRANE;
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE;
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
CURRENT FILING DATE: 2002-07-16
Prior Application removed - See File Wrapper or
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 330
LENGTH: 432
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Publication No. US20030162250A1
GENERAL INFORMATION:
        98.1%;
98.8%;
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Best Local Similarity 98.8%;
Matches 429; Conservative
Query Match
Best Local Similarity 98.8
Matches 429; Conservative
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                                                                  CDGBLDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNW
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APPLICANT: Baker, Kevin P.

APPLICANT: Baker, Kevin P.

APPLICANT: Betstein, David

APPLICANT: Eaton, Dan 1.

APPLICANT: Ferrara, Napoleone

APPLICANT: Ferrara, Napoleone

APPLICANT: Godowski, Paul J.

APPLICANT: Hillan, Kenneth J.

APPLICANT: Pan, James

APPLICANT: Poll James

APPLICANT: Pan, James

APPLICANT: 
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APPLICATION NUMBER: 60/099536
FILING DATE: 1998-09-09
APPLICATION NUMBER: 60/099596
FILING DATE: 1998-09-09
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US-10-015-392A-275
; Sequence 275, Application US
; Publication No. US200301669f
~~MRRAL INFORMATION:
RAKET, Kevin P.
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Pred. No. 6.1e-222;
0; Mismatches 0; Indels 5;
                                                    or
                                                 See File Wrapper
PRIOR APPLICATION NUMBER: 60/099598
PRIOR FILING DATE: 1998-09-09
Remaining Prior Application data removed
NUMBER OF SEQ ID NOS: 477
SEQ ID NO 275
LENGTH: 432
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ilarity 98.8%;
Conservative C
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; ORGANISM: Homo sapiens
US-10-015-392A-275
                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 429; Conser
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5.1.6 Compugen Ltd version - 2003 ( GenCore (c) 1993 Copyright

model SK - protein search OM protein

2003, 07:45:50 November 23 Run on:

; Search time 28.7208 Seconds (without alignments) 1456.555 Million cell updates/sec

US-09-607-745-2 2342 1 MDPDSDQPLNSLDVKPLRKP. score: Sequence: Title: Perfect

.....VYTKVSAYLNWIYNVWKAEL

BLOSUM62 Gapop 10.0 Scoring table:

96168682 residues Gapext 0.5 283308 segs, Searched:

Total number of hits satisfying chosen parameters:

283308

Minimum DB seg length: 0 Maximum DB seg length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 76:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	hepsin (EC 3.4.21.	enteropeptidase (E	enteropeptidase (E	hepsin (BC 3.4.21.	Ω.			1 (EC 3.	polyprotein - Afri	(EC 3.	acrosin (EC 3.4.21	acrosin (EC 3.4.21		low-density lipopr		(EC	membrane-bound arg	brain-specific ser	acrosin (EC 3.4.21	~	chymotrypsin (EC 3	trypsin (EC 3.4.21	(EC 3.4.	tion fac	plasmin (EC 3.4.21	sin (E	plasmin (EC 3.4.21	tasin (E	plasmin (EC 3.4.21
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## ALIGNMENTS

transmembrane doma Accession: 4.21.-) - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Decies: 31-02-1988 #sequence\_revision 31-Dec-1988 #text\_change 18-Jun-1999
C;Accession: S00845
R;Leytus, S.P.; Loeb, K.R.; Hagen, F.S.; Kurachi, K.; Davie, E.W.
Biochemistry 27, 1067-1074, 1988
A;Title: A novel trypsin-like serine protease (hepsin) with a putative transment A;Reference number: S00845; MUID:88209431; PMID:2835076
A;Accession: S00845
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Cross-references: EMBL:X07732; NID:g32063; PIDN:CAA30558.1; PID:g32064
C;Genetics:
A;Gene: GDB:HPN; TMPRSS1; hepsin
A;Cross-references: GDB:135685; OMIM:142440
A;Gene: GDB:HPN; TMPRSS1; hepsin
A;Cross-references: GDB:135685; OMIM:142440
C;Keywords: hydrolase; liver; serine proteinase; transmembrane protein
F;23-45/Domain: trypsin homology
C;Keywords: hydrolase; liver; serine proteinase; transmembrane #status predicted
F;133-400/Domain: trypsin homology cTRY>
F;183-204,291-359,322-338,349-381/Disulfide bonds: #status predicted
F;203,257,353/Active site: His, Asp, Ser #status predicted 11; 138 183 142 242 293 262 202 78 4 5 9 ----SQELRMRNSSGPCLS 19 KPRIPMETFRKVGIPIIIALLSLASIIIVVVLIKVILDKYYFLCGQPLHFIPRKQLCDGE HCFRKHTDVFN-WKVRAGSDKLGSFPSLAVAKIIIIEFNPMYP------KDNDIALMK LDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNWFSACFDNFTEALAETAC 91 BEMGF-----LRAL---THSELDVRTAGANGTSGFFCVDEGRLPHTORLLEVISVCDCPR LQFPLTFSGTVRPICLPFFDEELTPATPLWIIGWGFTKQNGGKMSDILLQASVQVIDSTR GSLVSLHCLACG-KSLKTPRVVGGEEASVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAA Gaps 83; 417; DB 1; Length Indels 161; Similarity 31.5%; Score 584.5; DB 1 Similarity 31.5%; Pred. No. 7.2e-41; 0; Conservative 60; Mismatches 161 :::: | | | | | :::
15 RPKVAALT---AGTLLLITAIGAASWAIVAVLLR-ROMGYSSKPTFRAVEIGPDQDLDVVEITEN----Query Match Best Local Simi Matches 140; 79 139 184 294 263 46 143 243 심 à 입 d 7 g δ 셤 δ  $\delta$ 

QY 165ITENSQELRMRNSSGPCLSGSLVSLHCLACGKSLKTPRVVGGEEASVDSW 214	QY 329 FTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPEGGVDTCQGDSGGP 388	A43090 enteropeptidase (EC 3.4.21.9) precursor [validated] - bovine N;Alternate names: enterokinase C;Species: Bos primigenius taurus (cattle) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 28-Apr-2003 C;Accession: A43090; A48874; A61436 R;Kitamoto, Y.; Yuan, X.; Wu, Q.; McCourt, D.W.; Sadler, J.E. Proc. Natl. Acad. Sci. U.S.A. 91, 7588-7592, 1994 A;Title: Enterokinase, the initiator of intestinal digestion, is a mosaic protease compose A;Reference number: A43090; MUID:94329561; PMID:8052624 A;Accession: A43090 A;Status: nucleic acid sequence not shown; translated from GB/EMBL/DDBJ A;Molecule type: mRNA	V UU 'O Z	A; Residues: 801-1035 <lav> A; Residues: 801-1035 <lav> A; Cross-references: GB:L19663; NID:g416131; PIDN:AAA16035.1; PID:g416132 A; Note: parts of this sequence, including the amino end of the mature protein, were confired; A; Note: parts of this sequence, including the amino end of the mature protein, were confired; A; Light, A; Janska, H.  J. Protein Chem. 10, 475-480, 1991 A; Title: The amino-terminal sequence of the catalytic subunit of bovine enterokinase. A; Reference number: A61436; MUID:92189715; PMID:1799406 A; Accession: A61436; MUID:92189715; PMID:1799406</lav></lav>	y'', 809-827 <lig> 'Y', 909-827 <lig> 'Y', 909-827 <lig> 'Y', 909-827 <lig> 'Y', 909-827 <lig 'y',="" 909-827="" 909<="" <lig="" th=""><th>A; Description: cleaves propeptide from trypsinogen to produce active trypsin A; Pathway: intestinal digestive hydrolase cascade C; Superfamily: enteropeptidase; Cir/Cis repeat homology; LDL receptor ligand-binding repe C; Keywords: glycoprotein; hydrolase; intestine; serine proteinase; transmembrane protein; F; 22-38/Domain: transmembrane #status predicted <twm> F; 22-117/Product: enteropeptidase mini chain #status predicted <mch> F; 118-800/Product: enteropeptidase heavy chain #status predicted <hch> F; 119-236/Domain: LDL receptor ligand-binding repeat homology <ldl1> F; 554-647/Domain: Cir/Cis repeat homology <cir> F; 554-647/Domain: LDL receptor ligand-binding repeat homology *LDL2&gt; F; 659-693/Domain: LDL receptor cysteine-rich domain homology #status atypical <srcf #status="" 801-1035="" <lch="" chain="" enteropeptidase="" f;="" light="" predicted="" product:=""></srcf></cir></ldl1></hch></mch></twm></th></lig></lig></lig></lig></lig>	A; Description: cleaves propeptide from trypsinogen to produce active trypsin A; Pathway: intestinal digestive hydrolase cascade C; Superfamily: enteropeptidase; Cir/Cis repeat homology; LDL receptor ligand-binding repe C; Keywords: glycoprotein; hydrolase; intestine; serine proteinase; transmembrane protein; F; 22-38/Domain: transmembrane #status predicted <twm> F; 22-117/Product: enteropeptidase mini chain #status predicted <mch> F; 118-800/Product: enteropeptidase heavy chain #status predicted <hch> F; 119-236/Domain: LDL receptor ligand-binding repeat homology <ldl1> F; 554-647/Domain: Cir/Cis repeat homology <cir> F; 554-647/Domain: LDL receptor ligand-binding repeat homology *LDL2&gt; F; 659-693/Domain: LDL receptor cysteine-rich domain homology #status atypical <srcf #status="" 801-1035="" <lch="" chain="" enteropeptidase="" f;="" light="" predicted="" product:=""></srcf></cir></ldl1></hch></mch></twm>
Qy 354 CNADDAYQGEVTEKMMCAGIPEGGVDTCQGDSGGPLMYQSDQMHVVGIVSWGYGC 408	A56318 enteropeptidase (EC 3.4.21.9) precursor [validated] - human N;Alternate names: enterokinase C;Species: Homo sapiens (man) C;Date: 19-May-1995 #sequence_revision 09-Aug-1996 #text_change 28-Apr-2003 C;Accession: A56318; B43090 R;Kitamoto, Y.; Veile, R.A.; Donis-Keller, H.; Sadler, J.E. Biochemistry 34, 4562-4568, 1995 A;Title: cDNA sequence and chromosomal localization of human enterokinase, the proteolyt A;Reference number: A56318; MUID:95234679; PMID:7718557 A;Accession: A56318	860; NID:g746412; PIDN Wu, Q.; McCourt, D.W.; .A. 91, 7588-7592, 199 initiator of intestin ; MUID:94329561; PMID: uence not shown 860 f association with the	-terminal myristoylation of the heavy chain. 083; OMIM:226200 tidase is variously reported to contain two (heavy sibly, conversion from membrane-bound to soluble f	~ + 10 MM L + U U	F;643-677/Domain: Life to the control of the contro	

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Accession: A53663

Righterate names: entercokinase

G/Species: Sins scrofa domestica (domestic pig)

G/Species: A53663

R/Mtsushima, M.; Ichinose, M.; Yabagi, N.; Kakei, N.; Tsukada, S.; Miki, K.; Kurokawa, I.

A/Title: Gructural daracerization of porcine enteropeptidase.

A/Residues: A53663

A/Accession: A53679

A/Accession: A53663

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                                                                                                         --CPRGRFLTATCQDCGRRKLPVDRIVGGQDSSLGRWPWQVSLRYDGTHLCGGSLLSGDW
                                                                                                                                                                                                           IALMKLQFPLTFSGTVRPICLPFFDEELTPATFLWIIGWGFTKQNGGKMSDILLQASVQV
                                                                                GPCLSGSLVSLHCLACG-KSLKTPRVVGGEEASVDSWPWQVSIQYDKQHVCGGSILDPHW
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                              EEMGFLRALAHSELDVRTAGANGTSGFFCVDEGGLPLAQRLLDVISVCD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WGYGCGGPSTPGVYTKVSAYLNWIYNVWK
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WGTGCALARKPGVYTKVIDFREWIFQAIK
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Best Local (
Matches 12'
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';801-1030/Domain: trypsin homology <TRY>
';116,147,170,194,233,263,264,404,456,486,519,550,646,698,722,741,762,864,903,965/Bindin
';788-912,826-842,926-993,957-972,983-1011/Disulfide bonds: #status predicted
';841,892,987/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             surface serine proteinase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IALMKLOFPLTFSGTVRPICLPFFDEELTPATPLWIIGWGFTKQNGGKMSDILLQASVQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-Jan-1995 #text_change 18-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IDSTRCNADDAYQGEVTEKMMCAGIPEGGVDTCQGDSGGPLMYQ-SDQWHVVGIVSWGYG
                                                                                                                                                                                                                                                       CLSGSLVSLHC--LACGKSLKT----PRVVGGEBASVDSWPWQVSIQYDKQHVCGGSILD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLEDSLILLQCNYKSCGKKLVTQEVSPKIVGGSDSREGAWPWVVALYFDDQQVCGASLVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNWFSACFDNFTEALAETAC
                                                                                                                                                                                                                          IPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNWFSACFDN
                                                                                                                                                                                                                                                                                                                            --ITENSQELRMRNSSGP
                                                                                                                                                                                                                                                                                                                                                         PHWVLTAAHC-FRKHTDVFNWKVRAGSDKLGSF--PSLAVAKIIIIEFNPMY---PKDND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL:X70900; NID:957928; PIDN:CAA50256.1; PID:957929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;162-399/Domain: trypsin homology <TRY>;187-203,290-358,321-337,348-380/Disulfide bonds: #status predicted;202,256,352/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 416;
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                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           $ sequence analysis of rat hepsin, a
$33777; MUID:93305733; PMID:8318546
                                                                                                                                                                                                                                                                                                                          FTEALAETACROMGY - - - - SSKPTFRAVEIGPDQDLDVVE-
                                                                                                                            4.4%; Score 571; DB 1; I 5.0%; Pred. No. 2.9e-39; ve 67; Mismatches 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             155;
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30.5%; Pred. No. 1.5e-39;
iive 64; Mismatches 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Y. N. Cross-references: EMBL:X70900; NID:g57928; FIUN
Y. Superfamily: hepsin; trypsin homology
7; Keywords: hydrolase; liver; serine proteinase;
7; 22-44/Domain: transmembrane #status predicted <
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LLFLTGIGAASWAIVTILLR-
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Species: Rattus norvegicus (Norway rat)
Date: 06-Jan-1995 #sequence_revision 06
Chacession: 833777; 832013
Richim. Biophys. Acta 1173, 350-352, 199
A;Title: Cloning and sequence analysis of
A;Reference number: 833777; MUID:93305733
A;Accession: 833777
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| CALPNRPGVYARVPRFTEWI 1030
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                                                                                                                                                 llarity 35.0%;
Conservative 6
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Best Local Similarity
Matches 137; Conser
                                                                                                                                             al Similarity
133; Conser
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RPKVAALT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-416 <FA
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Best Local S
Matches 133
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781 QCNHKSCGKKQVAC

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190

C-FRKHTDVFNWK

244 841

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LTFSGTVRPICLP

298

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PLASE Kallikrein (EC 3.4.21.34) precursor - mouse C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: A36557
R;Seidah, N.G.; Sawyer, N.; Hamelin, J.; Mion, P.; Beaubien, G.; Brachpapa, L.; Rochemont DNA Cell Biol. 9, 737-748, 1990
A;Title: Mouse plasma kallikrein: CDNA structure, enzyme characterization, and comparison A;Reference number: A36557
A;Molecule type: mRNA
A;Residues: 1-638 «SET:
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-638 «SET:
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;M
F;20-390/Product: plasma kallikreim mew, composite plasma kallikreim mew, composite sapple repeat cAP1>
F;20-109/Domain: apple repeat cAP2>
F;200-289/Domain: apple repeat cAP3>
F;200-289/Domain: apple repeat cAP4>
F;291-380/Domain: apple repeat cAP4>
F;291-638/Product: plasma kallikrein light chain #status experimental cMAT2>
F;391-631/Domain: trypsin homology cTRY>
F;391-621/Domain: trypsin homology cTRY>
F;391-621/Domain: trypsin homology cTRY>
F;21-104,47-77,51-57,111-194,137-166,141-147,201-284,227-256,231-237,292-375,318-347,322-F;21-104,47-77,51-57,111-194,137-166,141-147,201-284,227-256,231-237,292-375,318-347,322-F;127,215,308,453,459,494/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;396/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;434,483,578/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          290 EPCHF----KIYSGVAFEGEEINATFVQGADACQETCTKTIRCQFFTYSLLPQDCKAEGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99 AVAVRLSKDRSTLQVLDSATGNWFSACFDNFTEALAETACRQMGYSSKPTFRAVEIGPDQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               104;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              21.8%; Score 511; DB 1; Le
32.0%; Pred. No. 1.6e-34;
ive 62; Mismatches 106;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 128; Conserv
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in; duplication; fibrinolysis; glycoprotein; hydrolase; infla
ice #status predicted <SIG>
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A.Rocenie part of this sequence in Purification, Ma(2)-terminal sequencing and developm A.Rocenie type: procein
A.Rocenie part of this sequence in Purification, Ma(2)-terminal sequencing and developm A.Rocenie type: procein
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           --- FVKLNTAPNGSLILTASEQCFEDSLILL
     727 SDDVCQLLGLGTGNSSMPFFSSGG-GP
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C,Genetics:
A,Gene: PK
C,Superfamily: coagulation fac
C,Keywords: blood coagulation,
F;1-19/Domain: signal sequence

406

98

417 YTKVSAYLNWI 427

| : | : | | YARVPKFIEWI

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DAYQGEVTEKMMC

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F;21-104,47-77,51-57,111-194,137-166,141-147,201-284,227-256,231-237,292-375,318-347,322
F;127,215,308,396,494/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;434,483,578/Active site: His, Asp, Ser #status predicted
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C;Comment: Acrosin is an acrosomal protease that plays an important role in the initial
e-binding activity.
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1, Residues: 1-436 < WAT>
1, Cross-references: GB: S66245; NID: 9238706; PIDN: AAB20293.1; PID: 9238707
2, Kashiwabara, S.; Baba, T.; Takada, M.; Watanabe, K.; Yano, Y.; Arai, Y.
7. Biochem. 108, 785-791, 1990
1, Biochem. 108, 785-791, 1990
1, Fitle: Primary structure of mouse proacrosin deduced from the cDNA sequal to number: JX0138; MUID: 91185335; PMID: 2127931
                                                                                                                    1.7%; Score 508; DB 1; Length 638;
1.0%; Pred. No. 2.9e-34;
ve 45; Mismatches 82; Indels
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40.9%; Pred. No. 3.2e-34;
iive 37; Mismatches 90
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C; Date: 30-Sep-1991 #sequence_revision 30-Sep-1991
C; Accession: JX0172; JX0138
R; Watanabe, K.; Baba, T.; Kashiwabara, S.; Okamoto, J. Biochem. 109, 828-833, 1991
A; Title: Structure and organization of the mouse accesion: JX0172; MJID:92041732; PMID:193: A; Accession: JX0172
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WUID:91185335; PMIE
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Matches 112; Conser
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A; Molecule type: mRNA
A; Residues: 4-436 < XAS>
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C; Species: Xenopus laevis (African clawed frog)
C; Species: Xenopus laevis (African clawed frog)
C; Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 03-Feb-2003
C; Accession: T30337
R; Yang, J.C.; Lindsay, L.L.; Hedrick, J.L.
submitted to the EMBL Data Library, March 1998
A; Description: cDNA cloning of ovochymase, a chymotrypsin-like protease releases
A; Reference number: Z20829
A; Accession: T30337
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-1524 < YAN>
A; Residues: 1-1524 < YAN>
A; Cross-references: EMBL: U81290; NID: 92981640; PID: 92981641; PIDN: AAC24717.1
C; Superfamily: tryosin related polyprotein; trypsin homology
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A37344
acrosin (EC 3.4.21.10) precursor form 1 - mouse
C; Species: Mus musculus (house mouse)
C; Date: 19-Mar-1993 #sequence_revision 19-Mar-1993 #text_change 22-Jun-1999
C; Accession: A37344
R; Klemm, U.; Maier, W.M.; Tsaousidou, S.; Adham, I.M.; Willison, K.; Engel, Differentiation 42, 160-166, 1990
A; Title: Mouse preproacrosin: cDNA sequence, primary structure and postmeiot A; Reference number: A37344; MUID:90255839; PMID:2111255
A; Accession: A37344
A; Status: preliminary
A; Molecule type: mRNA
                                                                  : |: | : | | | | : | | | : | | | : | | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | : | | : | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
---VRAGSDKLGSFPSLA--VAKIIIIEFNPMYPKDNDIALMK
                                                                                                                                                                                                                    LOFPLIFSGTVRPICLPFFDEELTPATP -- LWIIGWGFTKONGGKMSDILLQASVQVIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRCNADDAYQGEVTEKMMCAGIPEGGVDTCQGDSGGPLMYQSD---QWHVVGIVSWGYGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             208 DLCNSTQWYNGRVTSTNVCAGYPEGKIDTCQGDSGGPLMCRDNVDSPFVVVGITSWGVGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              194 CGKSLKT-----PRVVGGEEASVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHCFRKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            249 TDVFNWKVRAGS-DKLGSFPSLAVAKIIIIEFNPMYPK---DNDIALMKLQFPLTFSGTV
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21.5%; Score 504.5; DB 2
Best Local Similarity 44.0%; Pred. No. 1.6e-33;
Matches 109; Conservative 38; Mismatches 86,
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255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           acrosin (EC 3.4.21.10) precursor - guinea pig (fragment)
C;Species: Cavia porcellus (guinea pig)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 22-Jun-1999
C;Accession: 829599
R;Gerton, G.L.; Hoff, H.B.; Baba, T.
submitted to the EMBL Data Library, May 1992
A;Description: The amino acid sequence of guinea pig proacrosin deduced from A;Reference number: 829599
A;Accession: 829599
A;Accession: S29599
A;Residues: 1-421 <GER>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      202 RVVGGEBASVDSWPWQVSIQY-----DKQHVCGGSILDPHWVLTAAHCFRKHTDVFNWK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---VRAGSDKLGSFPSLA--VAKIIIIEFNPMYPKDNDIALMKLOFPLTFSGTVRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ICLPFFDEELTPATP--LWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      102 LVFGAHEIEYGRNKFVKEPQQERYVQKIVIHEKYNAVTEGNDIALLKVTPPVTCGDFVGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TERMMCAGIPEGGVDICQGDSGGPLMYQSDQ---WHVVGIVSWGYGCGGPSTPGVYTKVS
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-----RIIGGQTAQPGAWPWMVSLQIFMAHNNRRY
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                                                                                                                                                                                                                                                                                                                                                                                                       437;
                                                                                                                                                                                                                                                                                                                                                                                                     Length
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              F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-43/Domain: acrosin light chain #status predicted <LCH>
F;43-286/Domain: trypsin howology <TRY>
F;44-437/Domain: acrosin heavy chain #status predicted <HCH>
F;22,211/Binding site: carbohydrate (Asn) (covalent) #status |
F;25-155,29-163/Disulfide bonds: #status predicted |
F;74-90/Disulfide bonds: #status predicted |
F;89,143,241/Active site: His, Asp, Ser #status predicted |
F;89,143,241/Active site: His, Asp, ser #status predicted |
F;178-247/Disulfide bonds: #status predicted |
F;210-226/Disulfide bonds: #status predicted |
F;237-267/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                             21.4%; Score 501.5; DB 2;
.larity 42.7%; Pred. No. 6.2e-34;
Conservative 35; Mismatches 85;
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Best Local Similarity
Matches 105; Conserv
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, 270-272, 1991
cDNA sequence, derived primary structure and phylogenetic
MUID:92031708; PMID:1932123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rat proacrosin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            s (Norway rat)
ce revision 31-Dec-1993 #text_change 22-Jun-1999
; Ā56620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       335 GKMSDILLQASVQVIDSTRCNADDAYQGEVTEKNMCAGIPEGGVDTCQGDSGGPLMYQSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 HACGGSLLNSHWVLTAAHCFDNKKKVYDWRLVFGAQEIEYGRNKPVKEPQEERYVQKIVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --VRAGSDKLGSFP--SLAVAKIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       les: 1-254,'LCDR',259,'DHEL',264,'GRLC',269-437 <KRE>
sequence modified after extraction from NCBI backbone
sequence extracted from NCBI backbone (NCBIN:89436, NCBIN:89439,
family: acrosin; trypsin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PID:957283
                                                                                                                                                                            predicted
                                                         PID:949858
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --PRVVGGEEASVDSWPWQVSIQY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nicontains: proactoring precursor - rac
Nicontains: proactoring
CiSpecies: Rattus norvegicus (Norway rat)
CiSpecies: 1318407; 330037; A56620
CiSteresion: S18407; Norman Acrosion: CDNA sequence, derived primary structus Astricle: Rat sperm acrosion: CDNA sequence, derived primary structus Astricle: Rat sperm acrosion: CDNA sequence, derived primary structus Astricle: Rat sperm acrosion: CDNA sequence, derived primary structus Astrossion: S18407; MUID:92031708; PMID:1932123
Astrossion: S18407; MUID:92031708; PMID:1932123
Astrossion: S18407; MUID:92031708; PMID:1932123
Astrossion: S30037
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Astrossion: Astrossion: Astrossion Structure and nucleotide sequence of the rat Astrossion: Astr
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 418;
A;Residues: 1-418 <KLE>
A;Cross-references: GB:X52466; NID:949857; PIDN:CAA36704.1; PID C;Superfamily: acrosin; trypsin homology
C;Superfamily: acrosin; trypsin homology
C;Keywords: glycoprotein; hydrolase; serine proteinase
F;39-283/Domain: trypsin homology <TRY>
F;18,208/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;21-151/Disulfide bonds: #status predicted
F;25-158/Disulfide bonds: #status predicted
F;70-86/Disulfide bonds: #status predicted
F;70-86/Disulfide bonds: #status predicted
F;175-244/Disulfide bonds: #status predicted
F;207-223/Disulfide bonds: #status predicted
F;234-264/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    serine proteinase; sperm;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 39.1%; Pred. No. 4.4e-34;
Matches 108; Conservative 36; Mismatches 90; Indels
                                                                                                                                                                          #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --- QWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWI 427
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C;Keywords: glycoprotein; hydrolase;
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acrosin (BC 3.4.21,10) precursor
N;Contains: proacrosin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        low-density lipoprotein receptor-related protein - mouse
() Species: Mus musculus (house mouse)
() Accession: JE0315
() Arcession: JE0315
() Biochem. 124, 784-789, 1938
() Arritle: A novel low-density lipoprotein receptor-related protein with type II memb)
() Arcession: JE0315
() Arcession: JE0315
() MulD:98429596; PMID:9756624
() Arcession: JE0315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGGSILDPHWVLTAAHCFRKHTDVFNWKVRAGSDKL---GSFPSLAVAKIIIIEFNPMYP
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A; Map position: 4935-4935
C; Superfamily: coagulation factor XI; trypsin homology
C; Superfamily: coagulation, duplication; fibrinolysis; glycoprotein; hydrolase; infla F; 1-19/Domain: signal sequence #status predicted <SIG>F; 20-638/Product: plasma kallikrein #status predicted <MAT>F; 20-109/Domain: plasma kallikrein heavy chain #status predicted <HCH>F; 20-109/Domain: apple repeat <API>F; 20-109/Domain: apple repeat <API
F; 20-109/Domain: apple r
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7;20-109/bowain: apple repeat <AP2>
7;210-199/bowain: apple repeat <AP3>
7;210-199/bowain: apple repeat <AP4>
7;210-289/bowain: apple repeat <AP4>
7;210-289/bowain: apple repeat <AP4>
7;21-380/bowain: apple repeat <AP4>
7;21-638/bowain: plasma kallikrein light chain #status predicted <LCH>
7;391-638/bowain: trypsin howology <TRY>
7;31-621/bowain: trypsin howology <TRY>
7;31-104,47-77,51-57,111-194,137-166,141-147,201-284,227-256,231-237,292-375,322-328,383
7;31-308,396,453,494/Binding site: carbohydrate (Asn) (covalent) #status experimental #status predicted
7:10-104,47-77,51-57,111-194,137-166,141-147,201-284,227-256,231-237,292-375,322-328,383
7:318-347,340-345/Disulfide bonds: #status predicted
7:10-104,47-77,51-57,51-57,111-194,137-166,141-147,201-284,227-256,231-237,292-375,322-328,383
7:318-347,340-345/Disulfide bonds: #status predicted
7:10-104,47-77,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,51-57,
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A; Residues: 20-27; 40-46, X', 48, 'H'; 50, 'X', 52-70, 'H'; 75-76, 'X', 78-80; 103-113; 131-140; 141-
A; Residues: 20-27; 40-46, 'X', 48, 'H'; 50, 'X', 52-70, 'H'; 75-76, 'X', 78-80; 103-113; 131-140; 141-
250-283, 'X', 285; 287-291, 'X', 293-295; 314-317, 'X', 319-320; 321-324; 'X', 329-333; 334-339, 'X'
525; 538-551; 562, 'X', 564-567; 573, 'X', 575-576; 578-583, 'X', 585; 592-604 cMCM>
C; Comment: This protein, synthesized in the liver, circulates as a noncovalent complex w
C; Comment: The zymogen is activated by factor XIIa, which cleaves the molecule into a liance linked by one or more disulfide bonds.
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C; Species: Homo sapiens (man)
C; Date: 13-Aug-1986 #sequence_revision 13-Aug-1986 #text_change 18-Jun-1999
C; Accession: A00921; A37939
R; Chung, D.W.; Fujikawa, K.; McMullen, B.A.; Davie, E.W.
Biochemistry 25, 2410-2417, 1986
A; Fitle: Human plasma prekallikrein, a zymogen to a serine protease that contains A; Reference number: A00921; MUD:86243359; PMID:3521732
A; Recession: A00921
A; Molecule type: mRNA
A; Residues: 1-638 < CHU>
A; Residues: 1-638 < CHU
A; Residues: 1-638 < 
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LIDLDLCNSTQWYNGRVMSTNVCAGYPEGKIDTCQGDSGGPLMCRDN 248
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42.2%; Pred. No. 6.8e+33;
ive 47; Mismatches 74;
                                                                                                                                                                                                     249 ANSPEVVVGITSWGVGCARAKRPGIYTATWDYLDWI
                                                                                                                                   393 -SDOWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWI
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Search completed: 1
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Hydroes the authors translated the codon AGG for residue 64 as Thr and CTG for residue R; Vazquez-Levin, M.H.; Reventos, J.; Gordon, J.W.

Eur. J. Biochem. 207, 23-26, 1992
A; Title: Molecular cloning, sequencing and restriction marr.
A; Reference number: $23499; MUID: 92331659.
                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: S12063

A; Receives inclear acid sequence not shown; translation not shown

A; Residues: 1-421 < VAZ>

A; Residues: 1-421 < VAZ>

A; Cross-references: EMBL:M77378

A; Cross-references: EMBL:M77378

A; Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1992

R; Keime, S.

Submitted to the EMBL Data Library, December 1989

A; Reference number: S12063

A; Reference number: S12063
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0970; NID:g28325; PIDN:CAA68784.1; PID:g28326
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Bj.20-42/Product: acrosin light chain #status predicted type: mrna

Fj.20-42/Product: acrosin heavy chain #status predicted

Fj.20-42/Product: acrosin heavy chain #status predicted

Fj.20-42/Product: acrosin heavy chain #status predicted

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Fj.30-42/Product: acrosin prodicted

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of human preproacrosin cDNA.
MUID:90128988; PMID:2298447
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A; Molecule type: DNA
A; Residues: 1-225,'R',227-421 <KEI2>
A; Cross-references: EMBL:X54017
B; Adham, I.M.; Klemm, U.; Maier, W.M.; Engel, W.
Hum. Genet. 84, 125-128, 1990
A; Title: Molecular cloning of human preproacrosin cDNA.
A; Reference number: A61022; MUID:90128988; PMID:2298447
A; Reference number: A61022, MUID:90128988; PMID:2298447
A; Reference number: A61022
A; Ratus: not compared with conceptual translation
A; Molecule type: mRNA
A; Residues: 1-63,'T', 65-225,'V',227-267,'R',269-421 <AD
B; Baba, T.; Watanabe, K.; Kashiwabara, S.I.; Arai, Y.
FEBS Lett. 244, 296-300, 1989
A; Title: Primary structure of human proacrosin deduced
A; Reference number: S03330; MUID:89153568; PMID:2493394
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P48038 oryctolagus	Q9bqr3 homo sapien	Q9y5y6 homo sapien	P35036 anopheles g	P07338 rattus norv	Q9es87 rattus norv	P20918 mus musculu	P35041 anopheles q	P06867 sus scrofa	P03951 homo sapien	O9esd1 mus musculu	P80009 canis famil	
ACRO RABIT	MPN HUMAN	ST14 HUMAN	TRY2 ANOGA	CTRB RAT	PSS8 RAT	PLMN MOUSE	TRY7 ANOGA	PLMN PIG	FA11 HUMAN	PSS8 MOUSE	PLMN_CANFA	
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34	35	36	37	38	6 8	40	41	42	43	44	45	

## ALIGNMENTS

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TISSUE=Pancreas;

WEDLINE=22388257, PubMed=12477932;

REDLINE=2388257, PubMed=12477932;

REDLINE=2388257, PubMed=12477932;

REDLINE=2388257, PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.L., Wang J., Hsieh F.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Carwinci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan R.J., Malek J.A., Gunarathe P.H.,

RA Bosak S.A., McEwan D.W., Sodergren E.J., Loguels R.A.,

RA Holton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnertion and initial analysis of more than 15,000 full-length
                                  TWS4 HUMAN STANDARD; PRT; 437 AA.

O9NRS4; O9NZA5;

16-OCT-2001 (Rel. 40, Last sequence update)

16-OCT-2003 (Rel. 42, Last annotation update)

Transmembrane protease, serine 4 (EC 3.4.21.-) (Membrane-type serine protease 2) (MT-SP2).
                                                                                                                                                                                                                                                                                                                    TISSUE=Pancreatic carcinoma;
MEDLINE=20283276; PubMed=10825129;
Mallrapp C., Haehnel S., Mueller-Pillasch F., Burghardt B.,
Iwamura T., Ruthenbuerger M., Lerch M.M., Adler G., Gress T.M.;
A novel transmembrane serine protease (TMPRSS3) overexpressed in pancreatic cancer.";
Cancer Res. 60:2602-2606(2000).
                                                                                                                                                                                                                       Craniata, Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Smeekens S.S., Lorimer D.D., Wang E., Hou J., Linnevers C.;
"MT-SP2, a novel type II membrane serine protease expressed in trachea, colon, and small intestine: identification, cloning, a chromosomal localization.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- FUNCTION: MAY PLAY A ROLE IN TUMOR PROGRESSION, METASTASIS
FORMATION AND TUMOR INVASION.
                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
                                                                                                                                                                                                     Homo sapiens (Human)
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                 HUMAN
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(Potential).
GASTRIC, COLORECTAL
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CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CLEAVAGE (POTENTIAL).
BY SIMILARITY.
CHARGE GECNAC. . . ) (POTENTIAL).
N-LINKED (GECNAC. . . ) (POTENTIAL).
MLODPDSDQPLNSLDVKPLRKPRIPMETFRK -> MSN
NPVSPWRPSES (IN REF. 2).
SUBCELLULAR LOCATION: Type II membrane protein (Poter TISSUE SPECIFICITY: HIGH LEVELS IN PANCREATIC, GASTR. AND AMPULLARY CANCER. VERY WEAK EXPRESSION IN NORMAL GASTROINTESTINAL AND UROGENITAL TRACT.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
SIMILARITY: Contains 1 SRCR domain.
SIMILARITY: Contains 1 LDL-receptor class A domain.
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EXTRACELLULAR (POTENTIAL)
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Query Match
Best Local Similarity 100.0%; Pred. No. 2.1e-195;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
2 DPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPIIIALLSLASIIIVVVLIKVILDKYYFL 61
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                        63
DPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPIIIALLSLASIIIVVVLIKVILDKYYFL
                                                                                                                                         FSACFDNFTEALAETACROMGYSSKPTFRAVEIGPDODLDVVEITENSOELRMRNSSGPC
                                                                                                                                                             124 FSACFDNFTEALAETACRQMGYSSKPTFRAVEIGPDQDLDVVEITENSQELRMRNSSGPC
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                                                             CGOPLHFIPRKOLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNW
                                                                                   CGQPLHFIPRKQLCDGBLDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNW
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBCELLULAR LOCATION: Type II membrane protein. Endoplasmic
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PubMed=12393794;
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-!- TISSUE SPECIFICITY: Expressed in the spiral ganglion, t supporting the organ of Corti and the stria vascularis.
-!- PTM: Undegoes autoproteolytic activation.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
-!- SIMILARITY: Contains 1 SRCR domain.
-!- SIMILARITY: Contains 1 LDL-receptor class A domain.
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EMBL; U75329; AAC51784.1;
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                            RMBL; AJ429216; CAD2137.1; -.

RMBL; AJ429216; CAD22137.1; -.

RMSP; P00761; IANI.

RMD; MGI:2155445; Tmprss3.

RILEFPRO; IPR001314; Chymotrypsin.

RILEFPRO; IPR001314; Chymotrypsin.

RILEFPRO; IPR00136; Ser_protease_Try.

RILEFPRO; IPR00190; Srcr_receptor.

REAT; PR0089; trypsin; 1.

RPRINTS; PR00722; CHYMOTRYPSIN.

RMART; SM00202; SR; 1.

RMART; SM00202; SR; 1.

RMART; SM00202; Tryp_SPc; 1.

RMART; SM00203; Tryp_SPc; 1.

RMART; SM00204; Tryp_SPc; 1.

RMART; SM00205; Tryp_SPc; 1.

RMART; SM00205; Tryp_SPc; 1.

RMART; SM00206; Tryp_SPc; 1.

RMART; M00206; Tryp_SPc; 1.

RMART; M00
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|ALILALA-----IGLGIHFDCSGKY--RCHSSFKCIELTARCDGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  246 RKHTDVFNWKVRAGSDKL,--GSFPSLAVAKIIIIEFNPMY-PK--DNDIALMKLQFPLTF
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SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
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-> H (IN REF. 1; CAC83350).
-> I (IN REF. 1; CAC83350).
IABCBFIOAF6E1EF6 CRC64;
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6.9%; Pred. No. 5e-52;
ve 72; Mismatches 153; Indels
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LDL-RECEPTOR CLASS A.
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BY SIMILARITY.

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   cense@isb-sib.ch)
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Best Local Similarity
Matches 161; Conser
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SEQUENCE FROM N.A., AND MUTAGENESIS.
MEDLINE=21139112; PubMed=11245484;
Afar D.B.H., Vivanco I., Hubert R.S., Kuo J., Chen E., Saffran D.C.,
Raitano A.B., Jakobovits A.;
"Catalytic cleavage of the androgen-regulated TMPRSS2 protease results in its secretion by prostate and prostate cancer epithelia.";
Cancer Res. 61:1686-1692(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDINE=21309069; PubMed=11414763; MEDINE=21309069; PubMed=11414763; Teng D.H., Chen Y., Lian L., Ha P.C., Tavtigian S.V., Wong A.K.; "Mutation analyses of 268 candidate genes in human tumor cell lines."; Genomics 74:352-364(2001).
SGTVRPICLPFFDEELTPATPLWIIGWGFTKONGGKMSDILLQASVQVIDSTRCNADDAY
                                      LMYQSDQ-WHVVGIVSWGYGCGGPSTPGVYTK
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MEDLINE=21104370; PubMed=11169526;
Vaarala M.H., Porvari K.S., Kellokumpu S., Kyllonen A.P., Vihko P.
"Expression of transmembrane serine protease TMPRSS2 in mouse and
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J. Pathol. 193:134-140(2001).
-!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ACTIVATED CLEAVAGE AND SECRETED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TMS2 HUMAN STANDARD; PRT; 492 AA.
015393; Q9BXX1;
15-JUL-1998 (Rel. 36, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Transmembrane protease, serine 2 precursor (EC 3.4.21.-)
TMPRSS2 OR PRSS10.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutei
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Paoloni-Giacobino A., Chen H., Peitsch M.C., Rossier
                                                                                                                                             QGEVTEKMMCAGIPEGGVDTCQGDSGGP1
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REMBL; AF123453; AAD37117.1; -.

REMBL; AF270487; AAX29280.1; -.

RESP; PO0763; 1DPO.

REROPS; S01.247; -.

REGNEW; MGC:11876; TMPRSS2.

RIM; 602060; -.

RIM; 70010254; Ser_proctease_Try.

RIM; REPROSTIZ; LDL, receptor_A.

RIM; REPROSTIZ; LDL, 1.

REPROSTIZ; REPROSTIZ; LDL, 1.

REPROSTIZ; RES0020; SR; 1.

REPROSTIZ; PS00202; SR; 1.

REPROSTIZ; PS00203; RRCR_2; 1.

REPROSTIZ; PS00204; RRYPSIN DOM; 1.

REPROSTIZ; PS00134; TRYPSIN LIS; 1.

REPROSTIZ; PS00135; TRYPSIN LIS; 1.
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SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
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CHARGE RELAY SYSTEM (BY SIMILARITY).
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CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM.
CLEAVAGE (POTENTIAL).
BY SIMILARITY.
CHARGE (BLONAC. .) (POTENTIAL).
N-LINKED (GLONAC. .) (POTENTIAL).
N-LINKED (GLONAC. .) (POTENTIAL).
K -> N (IN GDSNP:1056602).
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8.8%; Pred. No. 8.3e-51;
Ve 58; Mismatches 128; Indels 49
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MEDLINE=20521358; PubMed=11068177;
Underwood L.J., Shigemasa K., Tanimoto H., Beard J.B., Schneider E.N.,
Wang Y., Parmley T.H., O'Brien T.J.;
"Ovarian tumor cells express a novel multi-domain cell surface serine
                                                                                                                                                                                                                                                     408 QKCNSRYVYDNLITPAMICAGFLQGNVDSCQGDSGGPLVTSKNNIWWLIGDTSWGSGCAK
SGSLVSLHCLACGKSL---KTPRVVGGEBASVDSWPWQVSIQYDKQHVCGGSILDPHWVL
                  352 TRCNADDAYQGEVTEKMMCAGIPEGGVDTCQGDSGGPLMYQSDQ-WHVVGIVSWGYGCGG
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16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Transmembrane protease, serine 3 (EC 3.4.21.-) (Serine protease
TADG-12) (Tumor associated differentially-expressed gene-12 protein)
TMPRSS3 OR TADG12 OR ECHOS1.
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MEDLINE=21354482; PubMed=11462234;
Masmoudi S., Antonarakis S.E., Schwede T., Ghorbel A.M., Gratri M., Pappasavas M.P., Drira M., Elgaied-Boulila A., Wattenhofer M., Rossier C., Scott H.S., Ayadi H., Guipponi M.;
"Novel missense mutations of TMPRSS3 in two consanguineous Tunisian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORMS A; B AND D), AND VARIANT ILE-53.
MEDLINE=20578749; PubMed=11137999;
Scott H.S., Kudoh J., Wattenhofer M., Shibuya K., Berry A., Chrast Guipponi M., Wang J., Kawasaki K., Asakawa S., Minoshima S., Younus F., Mehdi S.Q., Radhakrishna U., Papasavvas M.P., Gehrig C., Rossier C., Korostishevsky M., Gal A., Shimizu N., Bonne-Tamir B., Antonarakis S.E.;
"Insertion of beta-satellite repeats identifies a transmembrane protease causing both congenital and childhood onset autosomal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                         411 PSTPGVYTKVSAYLNWIYNVWKAE 434
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      RANGE STANDER 
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                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21904597; PubMed=11907649; MATIANTS ASN-173 AND THR-426.
MEDLINE=21904597; PubMed=11907649; Wattenhofer M., Di lorio V., Rabionet R., Dougherty L., Pampanos A., Schwede T., Montserrat-Sentis B., Arbones L., Iliades T., Pampanos A., Pasquadibisceglie A., D'Amelio M., Alwan S., Rossier C., Dahl H.-H.M., Petersen M.B., Estivill X., Gasparini P., Scott H.S., Antonarakis S.E.; "Mutations in the TMPRSS3 gene are a rare cause of childhood nonsyndromic deafness in Caucasian patients."; J. Mol. Med. 80:124-131(2002).
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PTM: Undegoes autoproteolytic activation.
DISEASE: Defects in TMPRSS3 are a cause of childhood-onset autosomal recessive neurosensory deafness 8 (DFNB8) [MIM:601072] DISEASE: Defects in TMPRSS3 are a cause of congenital autosomal recessive neurosensory deafness 10 (DFNB10) [MIM:605316].
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
SIMILARITY: Contains 1 SRCR domain.
SIMILARITY: Contains 1 LDL-receptor class A domain.
                                                                                           ILE-53; SER-111 AND VAL-253.
MEDLINE-21317610; PubMed=11424922;
Ben-Yosef T., Wattenhofer M., Riazuddin S., Ahmed Z.M., Scott H.S., Kudoh J., Shibuya K., Antonarakis S.E., Bonne-Tamir B., Radhakrishna U., Naz S., Ahmed Z., Riazuddin S., Pandya A., Nance W.E., Wilcox E.R., Friedman T.B., Morell R.J.;
"Novel mutations of TMPRSS3 in four DFNB8/B10 families segregating congenital autosomal recessive deafness.";
J. Med. Genet. 38:396-400(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isold=P57727-3; Sequence=VSP 005392;
Name=T; Synonyms=Truncated, TADG-12V;
Isold=P57727-4; Sequence=VSP 005393, VSP 005394;
TISSUE SPECIFICITY: Expressed in many tissues including fetal cochlea. Isoform T is found at increased levels in some
                                                                                       TRP-109; PHE-194 AND ARG-407, AND VARIANTS
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SUBCELLULAR LOCATION: Type II membrane protein. Endoplasmic
    romic autosomal recessive deafness."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF201380; AAG37012.1; -...
EMBL; AB038157; BAB20077.1; -...
EMBL; AB038159; BAB20078.1; -...
EMBL; AB038159; BAB20080.1; -...
EMBL; AB038160; BAB20080.1; -...
HSSP; P00763; 1DPO.
MEROPS; S01.079; -...
Genew; HGNC:11877; TMPRSS3.
MIM; 605511; -...
MIM; 605511; -...
MIM; 605316; -...
GO; GO:0016021; C:integral to membrane; NAS.
GO; GO:0016021; C:integral to peptidolysis InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR002172; LDL_receptor_A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               dquence=VSP_005391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence=Displayed;
                                    2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRODUCT
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  non-synd
                                  Hum. Mutat. 18:101-108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=P57727-1;
Name=B; Synonyms=C
IsoId=P57727-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Event=Alternative
Name=A;
                                                                                       VARIANTS DFBN8/DFNB10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALTERNATIVE
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    with
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families
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HANDER BERNER BE

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CLEAVAGE (POTENTIAL).

BY SIMILARITY.

BY SIMI
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PRERADRRGRKLLCWRKPTKWKGPRPSHS (in isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY).
SIMILARITY).
SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                  Hydrolase; Serine protease; Transmembrane; Signal-anchor; Zymogen Endoplasmic reticulum; Deafness; Alternative splicing;
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C -> F (in DENBB/DENB10).

/FTIG=VAR_013494.

W -> C (in DENBB/DENB10).

/FTIG=VAR_011678.

I -> V (in dbSNP:2839500).

/FTIG=VAR_013101.

P -> L (in DFNBB/DFNB10).

/FTIG=VAR_013101.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EXTRACELLULAR (POTENTIAL)
LDL-RECEPTOR CLASS A.
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D -> G (in DFNB8/DFNB10)
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R -> W (in DFNB8/DFNB10)
/FTId=VAR_013491.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SERINE PROTEASE.
CHARGE RELAY SYSTEM (BY
CHARGE RELAY SYSTEM (BY
CHARGE RELAY SYSTEM (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL)
SIGNAL-ANCHOR (TYPE-II
(POTENTIAL).
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/FTId=VSP_005392.
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InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR001190; Srcr_receptor.
Pfam; PF00057; 1d1_recept_a; 1.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00192; LDLa; 1.
SMART; SM00202; SR; 1.
SMART; SM00202; SR; 1.
PROSITE; PS01209; LDLRA_1; 1.
PROSITE; PS01209; LDLRA_2; 1.
PROSITE; PS50068; LDLRA_2; 1.
PROSITE; PS50287; SRCR_1; FALSE_NEG.
PROSITE; PS50287; SRCR_2; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disease mutation; Polymorphism
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Last sequence update)
Last annotation update)
, serine 2 (EC 3.4.21.-) (Epitheliasin) (Plasmic
                                                                                                                                                                                                                                                                                                                                                                                                                EHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNWFSACFDNFTEALA
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                                                                                                                                                                                                                                                                                                                                           KSLKTPRVVGGEEASVDSWPWQVSIQYDKQHVCGGSILDPHWVLTA
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                                                                                                                                                                    IALLSLASIIIVVVLIKVILD---KY----YFLCGQPLHFIPRKQL
                                                                                                                                                                                                       IALILALA----IGLGIHFÖCSGKYRCRSSFKC---IBLIAR---
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                                                                                                                                Gaps
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MEDLINE=21104370; PubMed=11169526;
MEDLINE=21104370; PubMed=11169526;
MEDLINE=21104370; PubMed=11169526;
MEXPICESSION OF TRANSMEMBRANE SETINE Protease TMPRSS2 in mouse and human tissues.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1.1
                    A -> T.
/FTId=VAR_013496.
LKFFPIIVI -> FEVFSQSSSL (IN REF. 1).
                                                                                                                                63;
                                                                                             Length 454;
                                                                                          Score 660.5; DB 1; Length
Pred. No. 1e-49;
74; Mismatches 149; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protease X.";
the EMBL/GenBank/DDBJ
 FTId=VAR_013495
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Q9JIQ8; Q9JKC4; Q9QY82;
16-OCT-2001 (Rel. 40, Cre
16-OCT-2001 (Rel. 40, Las
28-FEB-2003 (Rel. 41, Las
Transmembrane protease, S
                                                                                          Query Match
Best Local Similarity 35.4
Matches 157; Conservative
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                       426
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STRAIN=BALB/c;
Jacquinet E.J., Ra
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                                                          CONFLICT
                        VARIANT
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CATALYTIC CHAIN.
CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-11 MEMBRANE PROTEIN)
(POTENTIAL).
EXTRACELULAR (POTENTIAL).
LDL-RECEPTOR CLASS A.
SRCR.
SERINE PROTEASE.
CHARGE RELAY SYSTEM (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "A novel mosaic serine protease, epitheliasin.";
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ACTIVATED BY
CLEAVAGE AND SECRETED (By similarity).
-!- TISSUE SPECIFICITY: EXPRESSED MAINLY IN PROSTATE AND KIDNEY.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
-!- SIMILARITY: Contains 1 SRCR domain.
-!- SIMILARITY: Contains 1 LDL-receptor class A domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ď
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TRANSMEMBRANE PROTEASE,
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                                                                             VLDSATGNWFSACFDNFTEALAETACROMGYSSKPTFRAVEIGPDOD--LDVVEITENSO 170
                                                                                                                                                                                             ELRMRNS---SGPCLSGSLVSLHCLACG-KSLK-TPRVVGGEEASVDSWPWQVSIQYDKQ 225
                                                                                                                                                                                                                                                                                                                                        VYSSQRKAWYPVCQDDWSESYGRAACKDMGY--KNNFYSSQGIPDQSGATSFMKLNVSSG 216
                                                                                                                                                                                                                                                                               NPMY----PKDNDIALMKLOFPLTFSGTVRPICLPFFDEELTPATPLWIIGWGFTKQNGGK
                                                                                                                                                                                                                                                                                                                         MSDILLQASVQVIDSTRCNADDAYQGEVTERMMCAGIPEGGVDTCQGDSGGPLM-YQSDQ
                                                                                                                                                                                                         HPNYDSKTKNNDIALMKLQTPLAFNDLVKPVCLPNPGMMLDLDQECWISGWGATYEK-GK
                                                                                                         -----FLCGQPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQ
                                                                                                                               SNCSTSEMECGSSGTCISSSLWCDGVAHCPNGEDENRC------VRLYGQSFILQ
                                                                                                                                                                                                                                      HVCGGSILDPHWVLTAAHCFR-----KHTDVFNWKVRAGSDKLGSFPSLAVAXIIIIEF
                                                               V-----GIPI-----IIALLSLASIIIVVVLIKVILDKYY-
                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 4).

TISSUE=Brain;

Mitsui S., Yamaguchi N.;

"Molecular cloning of mouse type 4 spinesin.";

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

-!- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
                                           59;
                       DB 1; Length 490;
                                                                                                                                                                                                                                                                                                                                                                                                                                           TMSS MOUSE STANDARD; PRT; 455 AA.
Q9ER02; Q9ER03;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Transmembrane protease, serine 5 (EC 3.4.21.-) (Spinesin)
TMPRSS5.
                     7%; Score 648.5; DB 1; Length
5.2%; Pred. No. 1.2e-48;
e 63; Mismatches 175; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       spinesin.";
the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VSP_005398;
07D2B03EA4D8A1A9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                KALRPGVYGNVTVFTDWIYQQMRA 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 splicing; Named isoforms=4;
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illarity 35.2
Conservative
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TISSUE=Brain;
Mitsui S., Yamaguchi N.;
"cDNA cloning of mouse st
Submitted (JUL-1998) to t
                                                               PLRKPRI PMETFRK
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Name=4;
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                    Query Match
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490 AA;
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GGLVEEAWKP -> MEAQVGLLWV (in isoform 1)

/FTId=VSP 005398.

D -> G (IN REF. 1; BAB20277).

5CFC31789C6899AA CRC64;
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SERGE.
SERGE SELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CLEAVAGE (POTENTIAL).
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
Missing (in isoform 2).
/FTId=VSP 005395.
Missing (in isoform 3).
/FTId=VSP 005396.
Missing (in isoform 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35;
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                                                                                                                                                                                                                                                                                                                                                                       EMBL; AB016229; BAB20276.1; ...

EMBL; AB016423; BAB20277.1; ...

EMBL; AB016423; BAB20277.1; ...

EMBL; AB041037; BAB40328.1; -..

EMBL; AB041037; BAB40328.1; -..

HSSP; P00763; 1DPO.

RESP; S01.313; -..

MGD; MGI:1933407; Tmprss5.

InterPro; IPR001254; Ser protease Try.

InterPro; IPR001254; Ser protease Try.

InterPro; IPR00190; Srcr_receptor.

RESPONDED: Trypsin; 1...

RESPONDED: TRYPSIN DOM; 1...

RESPONDED: TRYPSIN HIS; 1...

RESPONDED: TRYPSIN HIS; 1...

RECOITE; PS00135; TRYPSIN FRF; 1...

RECOITE; PS00420; SRCR 1; FALSE NEG.

RECOITE; PS00420; SRCR 1; FALSE NEG.

RECOITE; PS00420; SRCR 2; 1...

RECOITE; PS00420; SRCR 1; FALSE NEG.

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                                g
IsoId=Q9ER04-4; Sequence=VSP 005396; SIMILARITY: BELONGS TO PEPTIDASE FAMILY SIMILARITY: Contains 1 SRCR domain.
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MEDLINE=22388257; PubMed=12477932;

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Riausner R.D., Collins F.S., Wagner L., Shermen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Richards S.A., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Whiting M., Madan A., Young A.C., Shevchenko Y., Bourfard G.G.,

A Mhiting M., Madan A., Young A.C., Schwutz J., Myers R.M.,

Blakesley R.W., Touchman U.W., Green E.D., Dickson M.C.,

A Blakesley R.W., Touchman U.W., Green E.D., Dickson M.C.,

B Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

B Schnercfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.B.,

Cheneration and initial analysis of more than 15,000 full-length

A Human and mouse cDNA sequences."

A Human and mouse cDNA sequences."

A Human and mouse cDNA sequences."
                                                                                                       317
                                                                                                                                                               DAYQGEVTEKNMCAGIPEGGVDTCQGDSGGPLMYQS-DQWHVVGIVSWGYGCGGPSTPGV
VSLHCLACGKSLKTPRVVGGEEASVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHC--
                                                                                                                                           FDEELTPATPLWIIGWGFTKONGGKMSDILLQASVOVIDSTRCNAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
TISSUE=Liver;
MEDLINE=88209431; PubMed=2835076;
Leytus S.P., Loeb K.R., Hagen F.S., Kurachi K., Davie E.W.;
"A novel trypsin-like serine protease (hepsin) with a putative transmembrane domain expressed by human liver and hepatoma cells.";
Biochemistry 27:1067-1074(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata, Vertebrata, Euteleostomi,
Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T., le Beau M.M., Lemons R.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Serine protease hepsin (EC 3.4.21.-) (Transmembrane protease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'quences.";
U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                       417
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MEDLINE=91358502; PubMed=1885621;
Tsuji A., Torres-Rosado A., Arai '
Chou S.H., Kurachi K.;
                                                                     -FRKHTDVFNWKVRAGSDKLGS
                                                                                                                                                                                                                                                                                         429
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Bukaryota; Metazoa; Cho
Mammalia; Eutheria; Pri
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   e; Transmembrane; Signal-anchor.
SERINE PROTEASE HEPSIN, NON-CATALYTIC
CHAIN (POTENTIAL).
SERINE PROTEASE HEPSIN, CATALYTIC CHAIN
(POTENTIAL).
CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
EXTRACELLULAR (POTENTIAL).
SERINE PROTEASE.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
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BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
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                                                                                                     MEDLINE=93348237; PubMed=8346233;
Torres-Rosado A., O'Shea K.S., Tsuji A., Chou S.H., Kurachi K.;
"Hepsin, a putative cell-surface serine protease, is required for mammalian cell growth.";
Proc. Natl. Acad. Sci. U.S.A. 90:7181-7187(1993).
-!- FUNCTION: Plays an essential role in cell growth and maintenance
                                                                                                                                                                                               of cell morphology.
-!- SUBCELLULAR LOCATION: Type II membrane protein.
-!- TISSUE SPECIFICITY: Present in most tissues, with the highest level in liver.
"Hepsin, a cell membrane-associated protease. Characterization, tissue distribution, and gene localization.";
J. Biol. Chem. 266:16948-16953(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 417;
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GO: 0005887; C:integral to plasma membrane; TAS.
GO; GO: 0008151; P:cell growth and/or maintenance; TAS.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser protease_Try.
Pfam; PF00089; trypsin; I.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
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Best Local Similarity 31.5%; Pred. No. 3.6e-43;
Matches 140; Conservative 60; Mismatches 161;
                                                                                                                                                                                                                                                          -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI
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EMBL; X07732; CAA30558.1; -.
EMBL; X07002; CAA30058.1; -.
EMBL; BC025716; AAH25716.1; -.
PIR; S00845; S00845.
HSSP; P00763; 1DPO.
MEROPS; S01.224; -.
Genew; HGNC:5155; HPN.
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EQUENCE FROM N.A.

MEDLINE=20289799; PubMed=10830953;

Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,

Hattori M., Fujiyama A., Ishii K., Totoki Y., Choi D.-K., Groner Y.,

A Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Groner Y.,

A Soeda E., Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K.,

A Polley A., Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,

Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W.,

Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,

Rosenthal A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,

A Shintani A., Sasaki T., Nordsiek G., Hornischer K., Brandt P.,

Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloecker H.,

Ramser J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E.,

"Ahrmever S., Borzym K., Gardiner K., Nizetic D., Francis F.,

"Ahrmever S., Borzym K., Gardiner K., Nizetic D., Francis F.,
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                                                   --SOELRMRNSSGPCLS 183

    --THSELDVRTAGANGTSGFFCVDEGRLPHTQRLLEVISVCDCPR 142

LQFPLTFSGTVRPICLPFFDEELTPATPLWIIGWGFTKQNGGKMSDILLQASVQVIDSTR
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MEDLINE=21606074; PubMed=11719902;
Holzinger A., Maier E.M., Buck C., Mayerhofer P.U., Kappler M.,
Haworth J.C., Moroz S.P., Hadorn H.-B., Sadler J.E., Roscher A.A.;
"Mutations in the proenteropeptidase gene are the molecular cause of congenital enteropeptidase deficiency.";
Am. J. Hum. Genet. 70:20-25(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Duodenum;
MEDLINE=95234679; PubMed=7718557;
Kitamoto Y., Veile R.A., Donis-Keller H., Sadler J.E.;
"cDNA sequence and chromosomal localization of human enterokinase, the proteolytic activator of trypsinogen.";
Blochemistry 34:4562-4568(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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or (EC 3.4.21.9) (Ente
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15-SEP-2003 (Rel. 42, La
Enteropeptidase precurso
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                                                                                                                                                  trypsinogen.

C. -:- SUBUNIT: HETERODIMER OF A CATALYTIC (LIGHT) CHAIN AND A MULTIDOMAIN (HEAVY) CHAIN LINKED BY A DISULFIDE BOND.

C. -:- SUBCELLULAR LOCATION: Type II membrane protein (Probable).

C. -:- TISSUE SPECIFICITY: INTESTINAL BRUSH BORDER.

C. -:- PTM: THE CHAINS ARE DERIVED FROM A SINGLE PRECURSOR THAT IS

C. -:- PTM: THE CHAINS ARE DERIVED FROM A SINGLE PRECURSOR THAT IS

C. -:- DISEASE: Defects in PRSS7 are a cause of enterokinase deficiency

(MIN:226200]; a life-threatening intestinal malabsorption disorder

c. -:- SIMILARITY: Contains 2 LDL-receptor class A domains.

C. -:- SIMILARITY: Contains 1 SEA domain.

C. -:- SIMILARITY: Contains 1 SRCR domain.

C. -:- SIMILARITY: Contains 1 SRCR domain.
                                    GO; GO:0005903; C:brush border; TAS. InterPro; IPR001314; Chymotrypsin. InterPro; IPR000859; CUB_domain. InterPro; IPR002172; LDL_receptor_A.
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HSSP, P00763; 1DPO.
MEROPS; S01.156; -.
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SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
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MYRISTATE (POTENTIAL).
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InterPro; IPR0000998; MAM domain.

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InterPro; IPR001254; SEA domain.

InterPro; IPR001254; SEA domain.

InterPro; IPR001251; CUB; 2.

InterPro; IPR00029; MAM; 1.

InterPro; Indl recept_a; 2.

InterPro; Indl recept_a; 2.

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67 HF-----IPRKQLCDGELDCPLGEDERHCVKSFPEGPAVAVRLSKDRSTLQVLDSATG 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PWQVSIQYDKQHVCGGSILDPHWVLTAAHC-FRKHTDVFNWKVRAGSDKLGSFPSLAVAK 273
                                                                                                                                                                                                                                                                                                                                                                                                                                  ---ITENSQELRMRNSSGPCLSGSLVSLHC--LACGKSLK----TPRVVGGEEASVDSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            687 NNGLVRFRIQSIWHTACAENWTTQISNDVCQLLGLGSGNSSKPIF-STDGGPFVKLNTAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                     274 III--IEFNPMY---PKDNDIALMKLQFPLTFSGTVRPICLPFFDEELTPATPLWIIGWG
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                                                                                                                                                                                                                                                                                                                            NLTDN-----
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                                                                                                                                             -> RENAKNEIDALSPIILIA
                                                                                                                                                                                                                                                         Gaps
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=99339944; PubMed=10411637; Kawamura S., Kurachi S., Deyashiki Y., Kurachi K.; "Complete nucleotide sequence, origin of isoform and functional characterization of the mouse hepsin gene."; Eur. J. Biochem. 262:755-764(1999).
               (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
    (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=98058912; PubMed=9395459; Vu T.-K.H., Liu R.W., Haaksma C., Tomasek J.J., Howard E.W.; "Identification and cloning of the membrane-associated serine"
                                                                                                                                                                                                                    Length 1019;
                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                B6AAA245F6D4A563 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protease, hepsin, from mouse preimplantation embryos."; J. Biol. Chem. 272:31315-31320(1997).
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                                                                                                                                                                                                                  Score 582.5; DB 1;
Pred. No. 1.7e-42;
62; Mismatches 132;
                                                                                                                                                                                                                                                                                                                            647 HPOCKNGECVPLVNLCDGHLHCEDGSDEADCVRFF----
N-LINKED (GLCNAC. N-LINKED (GLCNAC. N-LINKED (GLCNAC. N-LINKED (GLCNAC. N-LINKED (GLCNAC. N-LINKED (GLCNAC. N-LINKED (GLCNAC. Q -> E (IN REF. 3). S -> P (IN RRF. 3).
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                                                                                                                                                            (IN REF
                                                                                                                                                                                    112923 MW;
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                                                                                                                                                                                                                     24.9%;
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Conservative
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                      CARBOHYD
CARBOHYD
CARBOHYD
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                                                                                                            CONFLICT
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     CARBOHYD
                                                                           CARBOHYD
                                                                                           CARBOHYD
                                                                                                                                               CONFLICT
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                                                                                                        RA MEDLINE=2108560; Pubbaca=11217851;

RA MEDLINE=2108560; Pubbaca A., Shbata K., Konno H., Adachi J., Fukuda S.,

Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

Alzawa K., Izawa M., Mishi K., Riyosawa H., Kondo S., Yamanaka I.,

RA Azawa K., Izawa M., Mishi K., Riyosawa H., Kondo S., Yamanaka I.,

RA Adacha K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Satuli F., Suzuki R., Tomita M., Wagner I., Washio T.,

RA Shaik K., Deffelli D., Bother C., Fulita M., Gariboldi M.,

Gustinoich S., Hill D., Hofmann M., Anon H., Baldacelli R., Barsh G.,

Blake J., Boffelli D., Hoshima J., Mazzarelli J., Mombaerts P.,

Gustinoich S., Hill D., Hofmann M., Rodriguez I., Sakamoto N.,

RA Iyons P., Marchionni I., Mashima J., Mazzarelli J., Mombaerts P.,

Gustinoich S., Hill D., Hofmann M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.

RA Nordone P., Ring B., Kingwald M., Rodriguez I., Sakamoto N.,

Rasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.

Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Hayashizaki Y.,

Ruture 409:685-690(2001).

C. C. Subschick I. Toyo-oka K., Mang K.H., Weitz C., Whittaker C., Wilming L.,

Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Hayashizaki Y.,

Ruture 409:685-690(2001).

C. C. Subschick I. Toyo-oka K., Mang K.H., Weitz C., Wilming L.,

Ruture 409:685-690(2001).

C. C. Subschick I. Toyo-oka K., Mang K.H., Weitz C., Wilming I.,

Mane-1, Synonyms-la,

C. C. Subschick I. Toyo-oka K., Mang K.H., Weitz C.,

Rame-1, Synonyms-la,

C. C. Subschick I. Toyo-oka K., Mang K.H., Weitz C.,

Rame-1, Synonyms-la,

C. C. Subschick I. Menca isoforms-2;

Rame-2, Synonyms-2a,

C. Subschick I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN (POTENTIAL).
SERINE PROTEASE HEPSIN, CATALYTIC CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SERINE PROTEASE HEPSIN, NON-CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF030065; AAB84221.1; -...

R HSSP; P00763; 1DPO.

R MEROPS; S01.224; -..

R MGD; MGI:1196620; Hpn.

R MGD; MGI:1196620; Hpn.

InterPro; IPR001314; Chymotrypsin.

InterPro; IPR001254; Ser_protease_Try.

InterPro; IPR001264; Ser_protease_Try.

InterPro; IPR00120; Srr_receptor.

Pfam; PF00089; trypsin; 1.

PRINTS; PR00722; CHYMOTRYPSIN.

R SMART; SM00202; SR; 1.

SMART; SM00202; SR; 1.

R SMART; SM00202; Tryp SPc; 1.

R PROSITE; PS50240; TRYPSIN_DOM; 1.

R PROSITE; PS00134; TRYPSIN_HIS; 1.

R PROSITE; PS00135; TRYPSIN_HIS; 1.

R PROSITE; PS00135; TRYPSIN_SER; 1.
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EXTRACELLULAR (POTENTIAL)
SERINE PROTEASE.
[3]
SEQUENCE FROM N.A. (ISOFORM 1).
STRAIN=C57BL/6J; TISSUE=Kidney;
MEDLINE=21085660; Pubmed=112178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   249 TDVFN-WKVRAGSDKLGSFPSLAVAKIIIIEFNPMYP------KDNDIALMKLQFPLT
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                                                                                                                                                                                                                                                                                                                                                                                                                          90 CVKSFPEGPAVAVRLSKDRSTLQVLDSATGNWFSACFDNFTEALAETACROMGY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----PLYQVQLSPGDSRLAVLDKTEGTWRLLCSSRSNARVAGLGCEEMGFLRALAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----SSKPTFRAVEIG----PDQDLDVVEITENSQELRMRNSSGPCLSGSLVSL
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------CPRGRFLTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         288 LTEXIQPVCLPAAGQALVDGKVCTVTGWGNT-QFYGQQAMVLQEARVPIISNEVCNSPDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YQGEVTEKMMCAGIPEGGVDTCQGDSGGPLMYQ----SDQWHVVGIVSWGYGCGGPSTP
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CHARGE RELAY SYSTEM (BY SIMILARITY).
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BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
Missing (in isoform 2).
//FIG=VSP 007232.
L -> Y (IN REF. 3).
T -> Y (IN REF. 3).
G -> R (IN REF. 3).
NR -> ET (IN REF. 3).
P -> L (IN REF. 3).
H -> N (IN REF. 3).
H -> N (IN REF. 3).
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Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                               90;
                                                                                                                                                                                                                                                                                           Match 24.7%; Score 578; DB 1; Length 436; Local Similarity 31.1%; Pred. No. 1.4e-42; Les 136; Conservative 62; Mismatches 150; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TMS5 HUMAN STANDARD; PRT; 457 AA. Q9H3\overline{33}; 16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2003 (Rel. 41, Last annotation update)
Transmembrane protease, serine 5 (EC 3.4.21.-) (Spinesin)
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TISSUE=Brain;
PubMed=11741986;
Yamaguchi N., Okui A., Yamada T., Nakazato H., Mitsui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 SELDVRTAGANGTSGFFCVDEGGLPLAQRLLDVISVCD---
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42 VGTLLFLTGIGAASWAIVTILLQ------
                                                                                                                                                                                                                                                                                                                           62;
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                                                                                                                                                                                                                                                               46787 MW;
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204
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                                                                   DISULFID
                                                                                                                                  VARSPLIC
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IsoId=P98072-2; Sequence=VSP_005386;
                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                     Bovidae; Bovinae; Bos. NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Duodenum;
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                                                                                                                                    is copyright. It is produced through a collaboration titute of Bioinformatics and the EMBL outstation actics Institute. There are no restrictions on its nstitutions as long as its content is in no way ement is not removed. Usage by and for commercial cense agreement (See http://www.isb-sib.ch/announce/cense@isb-sib.ch).
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in the
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       cloned from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
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(POTENTIAL).
(POTENTIAL).
                            )6-6812(2002).
[ON: Type II membrane protein (Potential).
[Os. Brain-specific. Predominantly expressed axons, and at the synapses of motoneurons
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     novel transmembrane serine protease,
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CHARGE RELAY SYSTEM (BY SI
CLEAVAGE (POTENTIAL).
BY SIMILARITY.
CHARGE (GLCNAC. . . ) (PC
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64406AB4985A2651 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EXTRACELLULAR (POTENTIAL)
"Spinesin/TMPRSS5, a novel transmembrane serine p human spinal cord.";
J. Biol. Chem. 277:6806-6812(2002).
-!- SUBCELLULAR LOCATION: Type II membrane protei
-!- TISSUE SPECIFICITY: Brain-specific. Predomina neurons, in their axons, and at the synapses spinal cord.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.
-!- SIMILARITY: Contains 1 SRCR domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24.5%; Score 574; DB 1; 32.2%; Pred. No. 3.3e-42; ive 70; Mismatches 151.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, AB028140; BAB20375.1; -.
HSSP; P00763; 1DPO.
Genew; HGNC:14908; TMPRSSS.
MIM; 606751; -.
MEROPS; S01,313; -.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001190; Srcr_receptor.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp SPC; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
PROSITE; PS00420; SRCR_1; FALSE_NEG.
Hydrolase; Serine protease; Transmembr Glycoprotein.
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TRANSMEM 50 70 SIGNAL-AN
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Matches 129, Conservative
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J. Protein Chem. 10:475-480(1991).

-!- FUNCTION: RESPONSIBLE FOR INITIATING ACTIVATION OF PANCREATIC
-!- FUNCTION: RESPONSIBLE FOR INITIATING ACTIVATION OF PANCREATIC
PROTEOLYTIC PROBNZYMES (TRYPSIN, CHYMOTRYPSIN AND CARBOXYPEPTIDASE
A). IT CATALYZES THE CONVERSION OF TRYPSINOGEN TO TRYPSIN WHICH IN
TURN ACTIVATES OTHER PROBNZYMES INCLUDING CHYMOTRYPSINOGEN,
PROCARBOXYPEPTIDASES, AND PROBLASTASES.
-!- CATALYTIC ACTIVITY: Selective cleavage of 6-Lys-|-ile-7 bond in
QLSPRIGGFLEEAWQPRNN----CTSGQVVSLRCSECGARPLASRIVGGQSVAPGRWPWQA
                                                                                                      IEF---NPMYPKDN----DIALMKLQFPLTFSGTVRPICLPFFDEELTPATPLWIIGWGFT
                                                                                                                                                                                                                                                  331 KONGGKMSDILLQASVQVIDSTRCNADDAYOGEVTEKMMCAGIPEGGVDTCQGDSGGPLM
                                                                  SIQYDKQHVCGGSILDPHWVLTAAHCFR--KHTDVFNWKVRAGSDKLGSFPSLAVAKIII
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 801-1035 FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE=94043122; PubMed=8226855;
Lavallie E.R., Rehemtulla A., Racie L.A., Diblasio E.A.,
Ferenz C., Grant K.L., Light A., McCoy J.M.;
"Cloning and functional expression of a cDNA encoding the catalytic subunit of bovine enterokinase.";
J. Biol. Chem. 268:23311-23317(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bos taurus (Bovine).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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01-FEB-1996 (Rel. 33, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Enteropeptidase precursor (EC 3.4.21.9) (Enterokinase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Y-QSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYN
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SEQUENCE OF 801-827.
TISSUE=Intestine;
MEDLINE=92189715; PubMed=1799406;
Light A., Janska H.;
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                             CLEAVED BY A TRYPSIN-LIKE PROTEASE.

-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.

-!- SIMILARITY: Contains 2 LDL-receptor class A domains.

-!- SIMILARITY: Contains 1 SEA domain.

-!- SIMILARITY: Contains 1 SEA domain.

-!- SIMILARITY: Contains 1 SRCR domain.

-!- SIMILARITY: Contains 2 Logor domain.

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LDL-RECEPTOR CLASS
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- SIMILARITY: BELONGS TO

- SIMILARITY: Contains 2

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- SIMILARITY: Contains 1

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Id=VSP 005386.
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E207970B08296E13 CRC64;
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                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                      Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (FOIENTIAL).
CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                  growth and maintenance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATALYTIC CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SERINE PROTEASE.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                              surface serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LINKED (GLCNAC. ..) (POTENTIAL)
E5A9F8FA9550E180 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                            cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SERINE PROTEASE HEPSIN, (POTENTIAL).
                                                                                                                                                                                                                                                                        membrane protein.
                                                                                                                                                                                                                                                                      ON: Type II membrane prot
S TO PEPTIDASE PAMILY S1
                                                                                                                                                      SEQUENCE FROM N.A.
TISSUE=Liver;
MEDLINE=93305733; PubMed=8318546;
Farley D., Reymond F., Nick H.;
"Cloning and sequence analysis of rat hepsin,
                                                                                                                                                                                                                                 1173:350-352(1993).
essential role in cell
HEPS RAT STANDAKU; FRI, LOSSII; 005511; 01-FEB-1994 (Rel. 28, Created) 01-FEB-1994 (Rel. 28, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) Serine protease hepsin (EC 3.4.21.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24.3%; Score 568.5;
larity 30.5%; Pred. No. 8.8e
Conservative 64; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chymotrypsin.
Ser_protease_T
Srcr_receptor.
                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, X70900; CAA50256.1; -...
PIR, S33777; S33777.
HSSP; P00763; 1DPO.
MEROPS; S01.224; -...
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001190; Srcr_receptor.
Pfam; PR00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00202; SR, 1.
SMART; SM00202; SR, 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolase; Serine protease; Transme CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36 MW;
                                                                                                                                                                                                                     proteinase.";
Biochim. Biophys. Acta 1
-!- FUNCTION: Plays an e
of cell morphology.
-!- SUBCELLULAR LOCATION
-!- SIMILARITY: BELONGS
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2002
2002
2002
2003
3303
441
449
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43
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Best Local Similarity
Matches 137; Conser
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202
202
352
152
1852
187
111
4 111
7
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DOMAIN
ACT SITE
ACT SITE
ACT SITE
DISULFID
DISULFID
DISULFID
DISULFID
CARBOHYD
SEQUENCE
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TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
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MEDLINE=97224034; PubMed=9070615;

MEDLINE=97224034; PubMed=9070615;

MEDLINE=97224034; PubMed=9070615;

MEDLINE=97224034; PubMed=9070615;

A vasuoka S., Ohnishi T., Kawano S., Tsuchihashi S., Ogawara M.,

Masuda K.-I., Yamaoka K., Takahashi M., Sano T.;

Masuda K.-I., Yamaoka K., Takahashi M., Sano T.;

Trypsin-like protease found in the human airway.";

Am. J. Respir. Cell Mol. Biol. 16:300-308 (1997)

I m. J. Respir. Cell Mol. Biol. 16:300-308 (1997)

I m. J. Respir. Cell Mol. Biol. 16:300-308 (1997)

I m. J. Respir. Cell Mol. Biol. 16:300-308 (1997)

I m. J. Respir. Cell Mol. Biol. 16:300-308 (1997)

I con the mucous membrane independently of or in cooperation with other substances in airway mucous or bronchial secretions.

I chalyTIC ACTIVITY: Preferentially of or in cooperation with other substances at the Pl position of certain peptides, cleaving Boc-Phe-Ser-Arg-4-methylcoumaryl-7-amide most efficiently and having an optimum pH of 8.6 with this substrate.

I lucrophosphate, leupeptin, antipain, aprotinin, and soybean trypsin inhibitor at 10 microM.

I rypsin inhibitor at 10 microM.

I SUBCHILULAR LOCATION: TYPE II MEMBRANE PROTEIN. ACTIVATED BY CLEAVAGE AND SECRETED.

I TISSUE SPECIFICITY: Located in the cells of the submucosal serous
                                                                                                                           138
                                                                                                                                                                  237
                                                                                                                                                                                                           196
                                                                                                                                                                                                                                                     288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          375
LDCPLGEDBEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNWFSACFDNFTEALAETAC 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
S
                                                                                                                                                                                       --CPRGRFLTATCQDCGRRKLPVDRIVGGQDSSLGRWPWQVSLRYDGTHLCGGSLLSGDW
                                                                                                                                                             GPCLSGSLVSLHCLACG-KSLKTPRVVGGEEASVDSWPWQVSIQYDKQHVCGGSILDPHW
                                                                                                                                                                                                                                                                                                                              IALMKLQFPLTFSGTVRPICLPFFDEELTPATPLWIIGWGFTKQNGGKMSDILLQASVQV
                                                                                                                                                                                                                                                                                                                                                        257 IALVHLSSSLPLTEYIQPVCLPAAGQALVDGKVCTVTGWGNT-QFYGQQAVVLQEARVPI
                                                                                                                                                                                                                                                                                                                                                                                                                                        ----SDQE-----PLYQVQLSPGDSRLLVLDKTEGTWRLLCSSRSNARVAGLGC
                                                                                 -SSKPTFRAVEIG----PDQDLDVVEITENSQELRMRNSS
                                                                                                                                                                                                                                                       -----KDND
                                                                                                                                                                                                                                                                                      197 VLTAAHCFPERNRVLSRWRVFAGAVARTSPHAVQLGVQAVIYHGGYLPFRDPTIDENSND
                                                                                                                                                                                                                                                                                                                                                                                                                IDSTRCNADDAYQGEVTERMMCAGIPEGGVDTCQGDSGGPLMYQ----SDQWHVVGIVS
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MEDLINE=98234382; PubMed=9565616;
Yamaoka K., Masuda K.-I., Ogawa H., Takagi K., Umemoto N., Yasuoka
"Cloning and characterization of the cDNA for human airway trypsin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Euteleostomi;
                                                                                                                      90 BEMGFLRALAHSELDVRTAGANGTSGFFCVDEGGLPLAQRLLDVISVCD----
                                                                                                                                                                                                                                                VLTAAHCFRKHTDVFN-WKVRAGSDKLGSFPSLAVAKIIIIEFNPMYP---
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Airway trypsin-like protease precursor (EC 3.4.21.-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          404
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J. Biol. Chem. 273:11895-11901(1998)
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                                                                               139 RQMGY-
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HUMAN
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[PIIIALLSLASIIIVVVLIKVILDKYYFLCGQPLHFIPRKQLCDGE

| | : : | | | : : |: ---VGTLLFLTGIGAASWAIVTILLR-

KPRIPMETFRKVGJ

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:|:: RPKVAALT-

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                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOLIANIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
EXTRACELULAR (POTENTIAL).
SEA.
SERINE PROTEASE.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                 EMBL; AB002134; BAA28691.1; -.

R HSSP; P00750; 1RTF.

R MEROPS; S01.301; -.

R MIM; 605369; -.

GO; GO:0005876; C:extracellular; TAS.

GO; GO:0005837; C:integral to plasma membrane; TAS.

GO; GO:0005837; F:peptidase activity; TAS.

GO; GO:0005837; F:peptidase activity; TAS.

GO; GO:0005837; C:integral to plasma membrane; TAS.

GO; GO:0005837; F:peptidase activity; TAS.

R O; GO:0005837; F:peptidase activity; TAS.

R O; GO:0005837; F:peptidase.

R InterPro; IPR001314; Chymotrypsin.

R InterPro; IPR001254; SeA_domain.

R InterPro; IPR001254; SeA_domain.

R Pfam; PF001390; SEA; 1.

R PROSTTE; PS0024; SEA; 1.

R PROSITE; PS50240; TRYPSIN DOM; 1.

R PROSITE; PS00134; TRYPSIN DOM; 1.

R PROSITE; PS00135; TRYPSIN JER; 1.

R Hydrolase; Serine protease; Transmembrane; Signal-anchor; Zymu Glyconocytein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       418;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AIRWAY TRYPSIN-LIKE PROTEASE,
CATALYTIC CHAIN.
AIRWAY TRYPSIN-LIKE PROTEASE,
CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.3%; Score 568; DB 1; Length 41
2.4%; Pred. No. 9.8e-42;
ve 79; Mismatches 149; Indels
glands of the bronchi and trachea.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1-:- SIMILARITY: Contains 1 SEA domain.
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41
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DISULFID
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ACT_SITE
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TRANSMEM
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Best Local
Matches 13
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                                                                                                                                                                                      421
                         230 RSNSNPRDWIATSGIST--TFPKLRMRVRNILIHNNYKSATHENDIALVRLENSVTFTKD
                                                                                                                                                                                                            RKHTDVFNWKVRAGSDKLGSFPSL--AVAKIIIIEFNPMYPKDNDIALMKLQFPLTFSGT
                                                                                                                 364 VTEKMMCAGIPEGGVDTCQGDSGGPLMYQSDQ--WHVVGIVSWGYGCGGPSTPGVYTKVS
                                                                                         VRPICLPFFDEELTPATPLWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGE
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Sciurognathi, Muridae, Murinae, Mus
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-!- SUBCELLULAR LOCATION: Type II membrane protein (Probable).

-!- PTM: THE CHAINS ARE DERIVED FROM A SINGLE PRECURSOR THAT IS CLEAVED BY A TRYPSIN-LIKE PROTEASE (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.

-!- SIMILARITY: Contains 2 LDL-receptor class A domains.

-!- SIMILARITY: Contains 1 SEA domain.

-!- SIMILARITY: Contains 1 SEA domain.

-!- SIMILARITY: Contains 1 SRCR domain.

-!- SIMILARITY: Contains 1 MAM domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Enteropeptidase (EC 3.4.21.9) (Enterokinase).
PRSS7 OR ENTK.
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HSSP; Q07954; 1CR8.
MEROPS; S01.156; -.
MGD; MGI:1197523; Prss7.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR000859; CUB_domain.
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AYLDWI 412
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118735 M, LINKED (GLCNAC. . .) (POTI
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S6 N-LINKED (GLCNAC. . .) (POTI
99 N-LINKED (GLCNAC. . .) (POTI
118735 MW; E62549E463743C3D CRC64;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae,
                                                        23.6%; Score 552.5; DB 1;
larity 32.5%; Pred. No. 7.5e-40;
Conservative 71; Mismatches 150;
                                                                                                     701 IPLGNLCDSYPHCRDGSDEASCVRF---
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Matches 124
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SIGNAL-ANCHOR (TYPE-II MEMBRANE POTENTIAL).
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986 ISNEKCQ-QQLPEXNITESMICAGYEEGGIDSCQGDSGGPLMCQENNRWFLVGVTSFGVQ 1044
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SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
TISSUE=Duodenal mucosa;
MEDLINE=94327548; PubMed=8051081;
Matsushima M., Ichinose M., Yahagi N., Kakei N., Tsukada S.,
Miki K., Kurokawa K., Tashiro K., Shinomiya K.,
Miki K., Kurokawa K., Tashiro K., Shinomiya K.,
Miki K., Kurokawa K., Tashiro K.,
Miki K., Tashiro R., Shiokawa K., Shinomiya K.,
Miki K., Tashiro F., Takahashi T., Takahashi K.;
Miki K., Kurokawa K., Tashiro K.,
Miki K., Tashiro E.,
Miki M.,                                                                                                                                                                                                                                                                                                                                                                                                          12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 289 IALMKLOFPLIFSGTVRPICLPFFDEELTPATPLWIIGWGFTKONGGKMSDILLQASVQV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       235 PHWVLTAAHC-FRKHTDVFNWKVRAGSDKLGSFPSLAVAKIII--IEFNPMYP---KDND
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SUBCELLULAR LOCATION: Type II membrane protein (Probable).
PTM: THE CHAINS ARE DERIVED FROM A SINGLE PRECURSOR THAT IS CLEAVED BY A TRYPSIN-LIKE PROTEASE.
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P98074;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Enteropeptidase precursor (EC 3.4.21.9) (Enterokinase)
PRSS7 OR ENTK.
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Search completed: November 23, 2003, 07:49:48 Job time : 20.7538 secs
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LDL-RECEPTOR CLASS A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23.6%; Score 552; DB 1; Length 1034;
34.2%; Pred. No. 7.9e-40;
tive 69; Mismatches 141; Indels 34; Gaps
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Matches 127; Conservative
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Q96e86 homo sapien
Q8vca5 mus musculu
Q8cfe0 mus musculu
Q9bye2 homo sapien
Q8k1t0 mus musculu
Q9bye1 homo sapien
Q9dgr2 xenopus lae
Q8vde0 mus musculu
Q9ct73 homo sapien
Q9ct73 homo sapien
Q9ct73 rattus norv
Q8cj17 rattus norv
Q8cj17 rattus norv
Q8cj16 rattus norv
Q8cdr0 mus musculu
Q8cj16 rattus norv
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(without alignments)
1721.140 Million cell updates/sec
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2342
1 MDPDSDQPLNSLDVKPLRKP.....VYTKVSAYLNWIYNVWKAEL
GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_mammal:*
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Q9BYE2
Q8K1T0
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seg length: 200000000
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score greater than or equal
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Q9qyz9 mus musculu	Q9QYZ9	4	erl .	Ö	473.5	24.
Q9w7p9 paralichthy	Q9W7P9	m	260	20.2	473.5	
7	Q9JJI7	гH	TU:	ö	4	
	O9XZM7		581	Ö	476	42
Q9v4n6 drosophila	Q9V4N6		1379	Ö	477	41
sus sp. pre	029015	φ	-1	20.4	ω	40
09dqr1 xenopus lae	Q9DGR1	m	845	ö	479.5	39
Q96rz8 homo sapien	Q96RZ8		321	ö	481	38
Q8nf86 homo sapien	QSNF86		284		482.5	37
Q9pvx7	Q9PVX7	13	389	20.8	4,	36
Q8bz13	Q8BZ13		416			35
08bz30	Q8BZ30		416	0	486.5	34
O9r0w3 rati	Q9R0W3		812	0.	m	33
OSPWIO	Q8BM10		423	20.8	α	32
Q60491 Ca	Q60491	11	421	21.1	493.5	31
097506	097506		643	H.	496	30
O8bz10 mu	Q8BZ10		417	$\ddot{}$	498.5	29
P79343 bos taurus	P79343	9	377	ä	498.5	28
O8bike mus musculu	Q8BIK6	터	572	H	499.5	27
OE	Q8N171	4	327	21.3	499.5	26
	Q8BHM9	금	439	ä	501.5	25
OBrops mus misculu	Q8R0P5	11	638	Η.	502	24
enc	091674	13	1524	ä	504.5	23
8	Q9GL10	ω	329	ä	504.5	22
S	Q8VHK8	11	417	ä	523	21
	QBVDV1	11	417	22.3	523	20
4 ratt	090274	11	279	ς.	527	19
	QBIUBO	4	811	22.7	531	8
O8iue2 homo sapien	Q8IUE2	4	802	22.7	531	17

## ALIGNMENTS

RESULT 1

OGESSE

D 096ESS

D 096ESS

D 096ESS

D 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last amnotation update)

DE 01-MAR-2003 (TrEMBLrel. 23, Last amnotation update)

Similar to transmembrane procease, serine 4 (Fragment).

Similar to transmembrane procease, serine 4 (Fragment).

Mammalia; Eutheria; Primates; Craniata; Vertebrata; Buteleostomi; OC MCBL TaxID=9606;

NCBL TaxID=9606;

NCBL TaxID=9606;

NR C TISSUE-Enncreas;

RS STRUMLERHY: BELONGS TO PEPTIDASE FAMILY S1.

RS STRUMLED FROW N.A.

SUMMILE FROW N.A.

RS STRUMLARHY: BELONGS TO PEPTIDASE FAMILY S1.

DR HESP; POOT61; LAM1.

DR HESP; POOT61; LAM1.

DR HESP; POOT61; LAM1.

DR HESP; POOT62; AM112752.1; 
DR HESP; POOT62; LAM10.

DR HESP; POOT62; LAM10.

DR PRONIS; PROOT22; CAPACRYPSIN.

DR PRONIS; PROOT22; CAPACRYPSIN.

DR SMART; SMOOD20; TYPE SPC; 1.

DR RACKIE; PSOO134; TRYPSIN HIS; 1.

DR PROSITE; PSOO134; TRYPSIN HIS; 1.

DR PROSITE; PSOO135; TRYPSIN HIS; 1.

DR PROSITE; PSOO135; TRYPSIN HIS; 1.

NON TER 1.

NON TER 1.

SQUENCE 405 AA; 44474 MM; 951ACD52D9D48E04 CRC64;

us-09-607-745-2.rspt

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Page

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SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Breast tumor;
Strausberg R.;
Submitted (JAN-2003) to the EMBL/GenB
EMBL; BC042878; AAH42878.1; -.
Protease.
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471 AA; 52535 MW;
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                                                                                                                                                         FPEGPAVAVRLSKDRSTLQVLDSATGNWFSACFDNFTEALAETACRQMGYSSKPTFRAVE
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SEQUENCE FROM N.A.

Waddiaux G., Vallet V., Jaeger N.F., Hummler B., Rossier B.C.;

Waddiaux G., Vallet V., Jaeger N.F., Hummler B., Rossier B.C.;

Waddiaux G., Vallet V., Jaeger N.F., Hummler B., Rossier B.C.;

"Synergistic Activation of ENaC by Three Membrane-bound Channel-

"T activating Serine Proteases (mCAPI, mCAP2, and mCAP3) and Serum-

"T Glucocorticoid-regulated Kinase (GSKI) in Xenopus Oocytes.";

"T Gen. Physiol. 120:191-201(2002).

"T Gen. Physiol. 120:191-201(2002).

"T Gen. Physiol. ARRS307.1;

"T Gen. Physiol. ARRS307.1;

"T Gen. Physiol. ARRS307.1;

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"T Gen. Physiol. ARRS307.1;

"T Gen. Physiol. ARRS307.1;

"T Gen. Physiol. ARRS908.1;

                                                                                      FPEGPAVAVRLSKDRSTLQVLDSATGNWFSACFDNFTBALAETACROMGYSSKPTFRAVE
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                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ol-MAR-2002 (TrEMBLrel. 20, Created)

Ol-MAR-2002 (TrEMBLrel. 20, Last sequence update)

DE Similar to transmembrane protease, serine 4 (Channel-activating protease 2).

TMPRSS4.

Mus musculus (Mouse).

C Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Entheria, Rodentia, Sciurognath.

X NCBI_TaxID=10090;

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inae; Mus.
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    Length
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Query Match 92.5%; Score 2167; I Best Local Similarity 100.0%; Pred. No. 1.9 Matches 402; Conservative 0; Mismatches
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Strausberg R.;
Submitted (JAN-2002)
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tumor;
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Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                    Length
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PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
Hydrolase; Protease; Serine protease; Transmembrane.
SEQUENCE 435 AA; 47495 MW; DC52E45A43E01369 CRC64;
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OBCFEO;
O1-MAR-2003 (TrEMBLrel. 23, Created)
O1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
O1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to mosaic serine protease (Fragment).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae
                                                                                                                                                                              ch 18.7%; Score 1844; DB 11; Il Similarity 77.2%; Pred. No. 6.4e-171; 336; Conservative 43; Mismatches 56;
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  GELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNWFSACFDNFTEALAET
                                                              --VRFDWDKSLLKVYSGSSGEWLPVCSSSWNDTDSKR
                                                                                                                            ACROMGYSSKPIFRAVEIGPDQDLDVVEITENSQELRMRNSSGPCLSGSLVSLHCLACGK
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QTFGLNETCWITGFGKTKETDEKTSPFLREVQVNLIDFKKCNDYLVYDSYLTPRMMCAGD
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i; Hominidae;
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Last annotation u
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Catarrhini;
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Eukaryota; Metazoa; Cho:
Mammalia; Eutheria; Priv
NCBI_TaxID=9606;
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TCQQLGFDS--AYR
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Best Local Simi:
Matches 152; (
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        --PLH
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi,
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mu
NCBI_TaxID=10090;
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SEQUENCE FROM N.A.

STRAIN=citb-cj7;

Gulpponi M., Scamuffa N., Scott H.S., Antonarakis S.E.;

"Isolation of the mouse Tmprss3 genomic DNA sequence.";

Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.

-!-SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.

EMBL; AJ429216; CAD22137.1; -.

EMBL; AJ429216; CAD22137.1; -.

InterPro; IPR001314; Chymotrypsin.

R InterPro; IPR001254; Ser_protease_Try.

R InterPro; IPR001254; Ser_protease_Try.

R InterPro; IPR001254; Ser_protease_Try.

R Pfam; PF00089; trypsin; 1.

R PROMITS; PR00722; CHYWOTRYPSIN.

R SMART; SM00120; LDLa; 1.

R SMART; SM0020; SR; 1.

R SMART; SM0020; Tryp_SPC; 1.

R PROSITE; PS50046; LDLRA 1; 1.

R PROSITE; PS50247; SRCR 2; 1.

R PROSITE; PS50247; TRYPSIN DOM; 1.

R PROSITE; PS00135; TRYPSIN JSER; 1.

R PROSITE; PS00135; TRYPSIN JSER; 1.

R PROSITE; PS00135; TRYPSIN JSER; 1.

R PROSITE; PS00135; TRYPSIN JSER; 1.

R PROSITE; PS00135; TRYPSIN JSER; 1.

R PROSITE; PS00135; TRYPSIN JSER; 1.

R PROSITE; PS00135; TRYPSIN JSER; 1.

R PROSITE; PS00135; TRYPSIN JSER; 1.
IPMETFR--KVGIPIIIALLSLASIIIVVVLIKVILDKYYFLCGQ-
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(TrEMBLrel. 22, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
                                  01-OCT-2002 (TrEMBLrel. 22, Created)
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01-MAR-2003 (TrEMBLrel. 23, Last annot
Type II transmembrane serine protease.
TMPRSS3.
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                                                                                       -----VRVSGQRAALQVFTAAA--WRTMCSDDWKSHYAKIAC
                                    IALLSLASIIIVVVLIKVILD---KYYFLCGOPLHFIPRKOLCDGE
                                                                      LDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNWFSACFDNFTEALAETAC
                                                                                                        ----KPTFRAVEIGPDQDLDVVEITENSQELRMRNSSGPCLSGSL
                                                                                                                                         VSLHCLACG-KSLKTPRVVGGEBASVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHCF
                                                                                                                                                    RKHTDVFNWKVRAGSDKL--GSFPSLAVAKIIIIEFNPMY-PK--DNDIALMKLOFPLTF
                                                                                                                                                                                      260 YDLYHPKSWTVQVGLVSLMDSPVPSHLVEKII---YHSKYKPKRLGNDIALMKLSEPILF
                                                                                                                                                                                                                       BGGVDTCQGDSGGPLMYQSDQ-WHVVGIVSWGYGCGGPSTPGVYTK
                                                                                                                                                                                                                                                        SGTVRPICLPFFDEELTPATPLWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAY
                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                    Euteleostomi;
                   153; Indels
    Length
                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; E
Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
 Ore 687; DB 11
red. No. 4e-58;
Mismatches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          without a transmembrane domain from huma Biochim. Biophys. Acta 1518:204-209(2001]
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMEMBL; AB048797; BAB39742.1; -..
HSSP; P00763; 1DPO.
MEROPS; S01.087; -..
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001324; Ser_protease_Try.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR001190; Srcr_receptor.
Pfam; PF00089; trypsin; 1.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00192; LDLa; 1.
SMART; SM00202; SR; 1.
SMART; SM00202; SR; 1.
 Score
Pred.
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MSPS.
HOPO sapiens (Human).
Bukaryota; Metazoa; Chordata; Cr
Mammalia; Eutheria; Primates; Ca
NCBI_TaxID=9606;
9.3%; Sc
6.9%; Pre
ve 72;
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Q9BYE1,
01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
Mosaic serine protease.
29
illarity 36
Conservative
                                                                                     SDCKNAEDEYRC--
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436 ITSFLDWIHEQLER
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Query Match
Best Local Similarity
Matches 161, Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NWKVRAGSDKLGSFPSLA-VAKIIIBFNPMY---PKDNDIALMKLQFPLTFSGTVRPIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GWKVYAGTSNLHQLPEAASIAEIII---NSNYTDEEDDYDIALMRLSKPLTLSAHIHPAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LPFFDEELTPATPLWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKM
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
NCBI_TaxID=8355;
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                                                                                                                                                                                                               Indels
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolase; Protease, Serine protease.
SEQUENCE 537 AA; 58102 MW; A39FF4E8816DAECF CRC64;
                                                                                                                                                         Query Match 29.3%; Score 686.5; DB 4; Best Local Similarity 38.6%; Pred. No. 5.7e-58; Matches 142; Conservative 56; Mismatches 147;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence up)
01-MAR-2003 (TrEMBLrel. 23, Last annotation
Embryonic serine protease-2.
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Yamada K., Takabatake T., Takeshima K.;
"Isolation and characterization of threfrom Xenopus laevis.";
Gene 252:209-216(2000).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAIRSP; P00766; 1CHG.
MEROPS; S01.049; -.
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InterPro; IPR002172; LDL_receptor_A.
InterPro; IPR001254; Ser_protease_Try
Pfam; PF00057; ldl_recept_a; 4.
Pfam; PF00089; trypsin; 1.
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PRINTS; PR00261; LDLRECEPTOR.
SMART; SM00192; LDLa; 8.
SMART; SM00020; Tryp_SPC; 1.
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NCBI_TaxID=9606;
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                                                                                                                                                                                                                SGPCLSGSLVSLHCLACGKSLKT--PRVVGGEBASVDSWPWQVSIQYDKQHVCGGSILDP
                                                                                                                                                                                                                            HWVLTAAHC-PRKHTDVFNWKVRAGSDKLGSFPSLA---VAKIIIIEFNPMYPKDNDIAL
                                                                                                                                                                                                                                                                       MKLQFPLTFSGTVRPICLPFFDEELTPATPLWIIGWGFTKQNGGKMSDILLQASVQVIDS
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Sciurognathi, Muridae, Murinae, Mu
                                                                                                           23;
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TO PEPTIDASE FAMILY S1.
                                                                                      DB 13; Length
                                                                                   29.3%; Score 686.5; DB 13; Length
38.3%; Pred. No. 9.3e-58;
ive 58; Mismatches 153; Indels
PROSITE; PS01209; LDLRA 1; 8.
PROSITE; PS50068; LDLRA 2; 2.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
Hydrolase; Protease; Serine protease.
SEQUENCE 767 AA; 86001 MW; E0566A38796DE96E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
Last sequence update)
Last annotation update)
                                                                                                                                               GGSSVSCVLSSQWCDGVSDCPYGEDEMSCVSLYPAD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                453
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HSSP; P00761; 1AN1.

MGD; MGI:2155445; Tmprss3.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR00132; LDL_receptor_A.
InterPro; IPR001190; Srcr_receptor.
Pfam; PF00089; trypsin; 1.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00192; LDLa; 1.
SMART; SM00192; LDLa; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
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Best Local Similarity
Matches 145; Conserv
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01-MAR-2003
TMPRSS3 prot
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Q8VDE0;
01-MAR-2002
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; F
Mammalia; Butheria; Primates; Catarrhini; Hominidae;
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Last annotation update)
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                                                                                                                                                                                   Query Match
29.1%; Score 681; DB 11;
Best Local Similarity 36.9%; Pred. No. 1.5e-57;
Matches 161; Conservative 71; Mismatches 154;
PROSITE; PS50068; LDLRA_2; 1.
PROSITE; PS50287; SRCR_2; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolase; Protease; Serine protease.
SEQUENCE 453 AA; 49529 MW; 21E5697DC8781BD3
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Eur. J. Biochem. 268:2687-2699(2001).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SIEMBL; AF329454; AAK53559.1; -.
HSSP; P00761; 1AN1.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR002172; LDL_receptor_A.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR001264; Ser_protease_Try.
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MEDLINE=21223025; PubMed=11322890;
Jacquinet E., Rao N.V., Rao G.V., Wan
Holdal J.R.;
"Cloning and characterization of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
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O96T73;
O1-DEC-2001 (TrEMBLrel. 19, C
01-DEC-2001 (TrEMBLrel. 19, L
01-MAR-2003 (TrEMBLrel. 23, L
Epitheliasin.
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79 LDCPLGEDBEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNWFSACFDNFTEALAETAC
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135; Conser
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Best Local
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --KNNFYSSQ-----GIVDDSGSTSFMKLNTSAGNVDIYKKLYHSDACS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGSLVSLHCLACGKSL---KTPRVVGGEEASVDSWPWQVSIQYDKQHVCGGSILDPHWVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAAHCFRKH-TDVFNWKVRAGSDKLGSF----PSLAVAKIIIIEFNPMY---PKDNDIAL
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                               49;
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                                                                                                                                                                                                                                                 3ABA755BF276DADF CRC64,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                       28.6%; Score 670.5; DB 4;
.larity 38.5%; Pred. No. 1.8e<56;
Conservative 59; Mismatches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA
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Submitted (OCT-2001) to the BMBL/GenBank,
-!- SIMILARITY: BELONGS TO PEPTIDASE FAM:
EMBL; AB073550; BAB70683.1; -.
HSSP; P00761; 1AN1.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR00172; LDL_receptor_A.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR00190; Srcr_receptor.
Pfam; PF00057; ldl_recept_a; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        490
Pfam; PF00089; trypgin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00192; LDLa; 1.
SMART; SM00202; SR; 1.
SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS01209; LDLRA_1; 1.
PROSITE; PS50068; LDLRA_2; 1.
PROSITE; PS50287; SRCR_2; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
Hydrolase; Protease; Serine protease.
SEQUENCE 492 AA; 53863 MW; 3ABA755E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        468 AYRPGVYGNVMVFTDWIYRQMRAD 491
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(TrEMBLrel.
(TrEMBLrel.
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148; Conser
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RAACKDMGY
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01-DEC-2001 (
01-DEC-2001 (
01-MAR-2003 (
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Tsuzuki S
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Best Local S:
Matches 148
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TMPRSS2.
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Q920K3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSDSCSSRMVVSLRCIECGVRSVRRQSRIVGGSTASPGDWPWQVSLHVQGIHVCGGSIIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 FSACFDNFTEALAETACROMGYSSKPTFRAVEIGPDQ----DLDVVEITENSQEL-RMRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNDIALMKLQFPLTFSGTVRPICLPFFDEELTPATPLWIIGWGFTKQNGGKMSDILLQAS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                          36;
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STRAIN=NEDH;
Omer S., Bicknell A.B., Lowry P.J.;
Identification of a rat adrenal mitochondrial protease.";
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF537098; AAN06757.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27.2%; Score 636.5; DB 11; Length .1arity 36.2%; Pred. No. 3.3e-53; Conservative 62; Mismatches 141; Indels
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00192; LDLa; 1.
SMART; SM00202; SR; 1.
SMART; SM00202; SR; 1.
PROSITE; PS50068; LDLRA; 2; 1.
PROSITE; PS50287; SRCR 2; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
Hydrolase; Protease; Serine protease.
SEQUENCE 490 AA; 53518 MW; 2BC691551CAC409A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                   Length
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01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Adrenal mitochondrial protease long variant.
                                                                                                                                                                                                                                                                                                                                 Query Match
27.6%; Score 646; DB 11;
Best Local Similarity 38.8%; Pred. No. 4.4e-54;
Matches 151; Conservative 54; Mismatches 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            488
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                                                    DAYQGEVTEKMMCAGIPEGGVDTCQGDSGGPLMYQS-DQWHVVGIVSWGYGCGGPSTPGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BEHCVKSFPEGPA------VAVRLSKDRSTLQVLDSATGNWFSACFDNFTEALA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              Ower S., Bicknell A.B., Lowry P.J.;
"Identification of a rat adrenal mitochondrial protease.
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF537099; AAN06758.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                 Q8CJ16
Q8CJ16;
Q8CJ16;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Adrenal mitochondrial protease short variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 612; DB 11;
Pred. No. 6.2e-51;
62; Mismatches 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          371 AA; 40694 MW; 89A64081D9A1FE26
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RPGVYAKVAEFLDWIHD 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26.1%;
34.7%;
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O9DBIO;
01-JUN-2001 (TrEMBLrel. 17,
                                                                                                              YTKVSAYLNWIYN 429
                                                                                                                                | ||::||::
YAKVAEFLDWIHD 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 34.7
Matches 131; Conservative
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                                                                                                            417
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Q9DBIO
ID Q9DBI
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Q8CJ16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'DEELTPATPLWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNAD 357
-FRKHTDVFNWKVRAG---SDKLGSFPSLAVAKIIIIEFNPMYPKDN---DIALMKLQFP
                                                                                                                                                                                                                            LTFSGTVRPICLPFFDEELTPATPLWIIGWGFTKONGGKWSDILLQASVQVIDSTRCNAD
                                                                                                     VSLHCLACGKSLKTPRVVGGEEASVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHC--
                                                                                                                                                                                                                                                                                                        GIPEGGVDTCQGDSGGPLMYQS-DQWHVVGIVSWGYGCGGPSTPGV
                                                                            ----nrsoefaolsarpgslveeawopstncpsgri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79 LDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNWFSACFDNFTEALAETAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   187 VSLHCLACGKSLKTPRVVGGEEASVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHC--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SFRL-SRLSSWRVHAGLVSHGAVRQHQGTMVEKIIP----HPLYSAQNHDYDVALLQLRTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NL---SDIKL----NRSQBFAQLSARPGGLVEESWKPSANCPSGRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Phase I & II Team; on functional annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OBCDRO;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Transmembrane protease.
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .0%; Score 631.5; DB 11; Length 455; .2%; Pred. No. 1e-52; e 63; Mismatches 140; Indels 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.1; -.
69 MW; BE22EB2B7503C74B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          139 ROMGYSSKPTFRAVEIGPDQDLDVVEITENSQELRMRNS---
                                             ROMGYSSKPTFRAVEIGPDODLDVVEITENSQELRMRNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=C57B1/6J; TISSUE=Testis;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phi
"Analysis of the mouse transcriptome based on f
60,770 full-length cDNAs:";
Nature 420:563-573(2002).
EMBL; AK029714; BAC26577:1; -.
SEQUENCE 455 AA; 49669 MW; BE22EB2E7503C741
                                                                                                                                                                                                                                                                                                                                                                                                                                                          455
                                                                ::||
| SLGYFRLTQHKAVNL---SDIKL-
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                LSCPGVSSEEKLLP
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KSLGHIRLTQHKAVI
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                                                                                                                                                                                                                                                                                       DAYQGEVTERMMC
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Best Local S
Matches 135
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SEQUENCE FROM N.A.

STRAIN=C57BL/6J; TISSUE=Liver;

X Arakawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

X Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Aizawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A Aizawa K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

X Adota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

X Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

X Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

X Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

X Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

X Rodota K., Matsubi F., Suzuki R., Tomita M., Wagner L., Washio T.,

X Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

X Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

X Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

X Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,

X Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

X Byons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

X Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Stoketsuki S.,

X Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

X Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

X Hayashizaki Y.;

X Hayashizaki Y.;

X Hayashizaki Y.;

X Hayashizaki Y.;

X Hayashizaki Y.;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DSATGNWFSACFDNFTBALAETACRQMGYSSKPTFRAVEIGPDQDLDVVEITENSQELRM 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RNSSGPCLSGSLVSLHCLACGKSLKTPRVVGGEEASVDSWPWQVSIQYDKQHVCGGSILD 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FLCSVNGLCVP---ACDGIKDCPNGLDERNCVCRAMPQCQEDSTCISLPRVCDRQP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DCINGSDEEQCOEGVPCGTFTFQCEDRSCVKKP-----NPECD------
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
1300008A22Rik protein (RIKEN cDNA 1300008A22 gene).
TMPRSS6 OR 1300008A22RIK.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23.5%; Score 550.5; DB 11; Length 799; 33.2%; Pred. No. 1.8e-44; iive 60; Mismatches 146; Indels 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P. C. TISSUE-Liver;

Strausberg R.;

Strausberg R.;

Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

--- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.

EMBL; AK004939; BAB23684.1; --

EMBL; BC029645; AAH29645.1; --

READ; PRO0763; 1DPO.

READ; PRO01314; Chymotrypsin.

REAPER, PRO01314; Chymotrypsin.

REPPRO; IPR001314; Chymotrypsin.

REPRO; IPR001254; Ser_protease_Try.

READ; PR00089; trypsin; 1.

READ; PR00089; trypsin; 1.

READ; PR001254; Ser_protease_Try.

READ; PR00129; LDLRA_1; 1.

READ; PR00139; LDLRA_1; 1.

READ; PR01209; LDLRA_1; 1.

READ; PR01209; LDLRA_1; 1.

READ; PR01209; LDLRA_1; 1.

READ; PR011E; PS01209; LDLRA_1; 1.

READ; PR011E; PS01389; TRYPSIN HIS; 1.

READ; PROSITE; PS00134; TRYPSIN HIS; 1.

READ; PROSITE; PS00135; TRYPSIN ERR; 1.

READ; PROSITE; PS00135; TRYPSIN ERR; 1.

READ; PROSITE; PS00135; TRYPSIN ERR; 1.

READ; PROSITE; PS00135; TRYPSIN ERR; 1.

READ; PROSITE; PS00135; TRYPSIN ERR; 1.

READ; PROSITE; PS00135; TRYPSIN ERR; 1.

READ; PROSITE; PS00135; TRYPSIN ERR; 1.

READ; PROSITE; PS00135; TRYPSIN ERR; 1.

READ; PROSITE; PS00135; TRYPSIN ERR; 1.

READ; PROSITE; PS00135; TRYPSIN ERR; 1.

READ; PROSITE; PS00135; TRYPSIN ERR; 1.

READ; PROSITE; PS00135; TRYPSIN ERR; 1.

READ; PROSITE; PS00135; TRYPSIN ERR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Functional annotation of Nature 409:685-690(2001).
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Matches
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69 IPRKOLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLD-SATGNWFSACFD 127
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--GQSDCRDGS-DEQHC-DCGLQGLSSRIVGGTVSSEGEWPWQASLQIRGRHICGGALIA 596
                                                                                                                                                                                                                                                                                                              405
                                                                                                                                                                                                                                                                                                                                                                772
                                                                                   235 PHWVLTAAHCFRKHT-----DVFNWKVRAGSDKLGSFPSLAVAKIIIIEFNPMYPKDN 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=C57BL/6J; TISSUE=Thymus; MEDLINE=22354683; PubMed=12466851; The FANTOM Consortium, the RIKEN Genome Exploration Research Group Phase I & II Team; the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).

EMBL; AK038356; BAC29973.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               235 PHWVLTAAHC-FRKHTDVFNWKVRAGSDKLGSFPSLAVAKIII--IEFNPMYP---KDND
                                                                                                                                                                                                                                                                                                                                            410 IPLGNICDSYPHCRDGSDEASCVRF------INGTRSNNGLVQFNIHSIWHIACAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       128 NFTEALAETACROMGYSSKPTFRAVEI---GPDQDLDVVEITENSQELRMRNSSGPCLSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            460 NWTTQISNEVCHILGLGSANSSMPISSTGGGP----FVRVNQAPNGSLILTPSLQCSQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    288 DIALMKLOFPLIFSGTVRPICLPFFDEELTPATPLWIIGWGFTKQNGGKMSDILLQASVQ
                                                                                                                                                                                                                                   348 VIDSTRCNADDAYQGEVTEKMMCAGIPEGGVDTCQGDSGGPLMYQ--SDQWHVVGIVSWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38; Gaps
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 23.3%; Score 545; DB 11; Length 777; Local Similarity 32.5%; Pred. No. 5.9e-44; les 124; Conservative 72; Mismatches 148; Indels 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          777 AA; 87314 MW; A18E2F4ECF06D3A8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8CAN9;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Protease (Fragment).
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                          406 YGCGGPSTPGVYTKVSAYLNWIYNV 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                             773 LGCGRPNFFGVYTRVTRVINWIQQV 797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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Q8CAN9
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Search completed: November 23, 2003, 07:51:54
Tob time : 71.2201 secs

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                               SUMMARIES
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AX697206
BC012752
BC021368
AY043240
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                                                                                                                                                                                                                                                                                                                                                                                                             BC042878
4X149581
                                                                                                                                                                                                                                                                                                                                                                                                                                 AX190543
AX190546
AX149579
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Patent: WO 0104141-A 1 18-JAN-2001,
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Bandman,O., Hillman,J.L., Yue,H., Guegler,K.J., Corley,N.C.,
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Tang, Y.Tom, and
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                                                                                   BASE COUNT
ORIGIN
              TITLE
JOURNAL
FEATURES
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DS HOMEO Sapiens INC.

S HOMEO Sapiens INC.

PN JP 2002508970-A/6

PD 26-MAR-2002

PF 12-JAN-1999 JP 2000540252

PR 16-JAN-1998 US 09/008271

PI OLGA BANDMAN, JENNIFER L HILLMAN, HENRY YUE, KARL J GUEGLER, NEIL.

PI C CORLEY,

PI TOM Y TANG, PURVI SHAH

PC C12N15/09, A61K38/46, C07K16/40, C12N1/19, C12N1/21, C12N5/10 PC, C12N19/48, C12N9/64,

PC C12N15/09, A61K37/54, C12N5/00

CC 1337018

Location/Qualifiers

FH Key

Location/Qualifiers

FT source

//organism='Home sapiens (human)'.
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980 GACAAACTGGGCAGCTTCCCATCCCTGGCTGTGGCCAAGATCATCATCATTGAATTCAAC 1039
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16-JAN-1998 US 09/008271
OLGA BANDMAN, JENNIFER L HILLMAN, HENRY YUE, KARL J GUEGLER, NEIL
                                                                                                                                                     301 SerGlyThrValArgProlleCysLeuProPhePheAspGluGluLeuThrProAlaThr 320
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                                                   ProMetTyrProlysAspAspAspIleAlaLeuMetLysLeuGlnPheProLeuThrPhe 300
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1 (bases 1 to 2038)
Bandman,O., Hillman,J.L., Yue,H., Guegler,K.J., Corley,N.C., Tang,T.Y. and Shah,P.
Human protease molecule
Patent: JP 2002508970-A 6 26-MAR-2002;
INCYTE PHARMACEUTICALS INC
OS Homo sapiens (human)
PN JP 2002508970-A/6
PD 26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               401 IleValSerTrpGlyTyrGlyCysGlyGlyProSerThrProGlyValTyrThrLysVal
                                                                                 1040 CCCATGTACCCCAAAGACAATGACATCGCCCTCATGAAGCTGCAGTTCCCACTTTC
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/organism≂"Homo sapiens"
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_591 c 569 g 43
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JP 2002508970-A/6.
Homo sapiens (human)
Homo sapiens
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Length: Matches: Conservative Mismatches: Indels: Gaps:	2038)	LeuasnSerLeuaspVallysP: 	ysvalGlylleP 	albeullebysv            rccrcarcaagg	leProArglys6             TCCCGAGGAAGC	ii sCysvallyss                  !ACTGTGTCAAGA	SerThrieuGlnV 	heThrGluAlaI            TCACAGAAGCTO	heArgAlaValG              TCAGAGCTGTGG	sergingluleum	euHisCysLeuP             TGCACTGTCTTG	laServalAsps 	ilyGlyserllel             GAGGGAGCATCC	ThraspvalPher 	ceuAlaValAlai 	IealaLeumet  	7 7
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s: ity: larity:	2 (1-435)	MetaspProas            arggarccrga	ArgileProMe	Leualaseril            CTGGCGAGTAT	Leucysglygli            CTCTGCGGGCA	CysProLeuGl	AlavalArgle            GCAGTCCGCCT	TrpPheseral	MetGlyTyrSe             ATGGGCTACAG	AspvalvalGl            GATGTTGTTGA	Cysteusergl            TGTCTCTCAGG	ProArgValVa            ccccGTGTGGT	GlnTyrAspLy            CAGTACGACAA	AlaAlaHisCy            GCAGCCCACTG	AspLysLeuGl	ProMetTyrPr             CCCATGTACCC	- 12 - 12 - 12 - 12 - 12 - 12 - 12 - 12
ent Score; No.: t Similar: ocal Simi.	607-745-	1 200	260	41320	380	81	101	121	141	161	181	201	221	241	261	281	

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AF179224 20081 bp mRNA linear PRI 08-JUN-2000 Homo sapiens transmembrane serine protease 3 (TMPRSS3) mRNA, complete cds.
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AVRLSKDRSTLQVLDSATGNWFSACFDNFTEALAETACRQMGYSSKPTFRAVEIGPDQ
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IIIEFNPMYPKDNDIALMKLQPPLTFSGTVRPICLPFFDBELTPATPLWIIGWGFTKQ
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1100 TCAGGCACAGTCAGGCCCATCTGTCTGCTTTTGATGAGGAGCTCACTCCAGCCACC 1159
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

(bases 1 to 2081)

Wallrapp,C., Hahnel,S., Muller-Pillasch,F., Burghardt,B.,

Iwamura,T., Ruthenburger,M., Lerch,M.M., Adler,G. and Gress,T.M.

A novel transmembrane serine protease (TMPRSS3) overexpressed in pancreatic cancer
Cancer Res. 60 (10), 2602-2606 (2000)

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Wallrapp, C. and Gress, T.M.
Direct Submission
Submitted (20-AUG-1999) Internal Medicine I, University of Ulm,
Robert-Koch-Street 8, Ulm, Baden-Wuerttemberg 89081, Germany
Location/Qualifiers
                                                                                                                            341 LeuLeuGlnAlaSerValGlnVallleAspSerThrArgCysAsnAlaAspAspAlaTyr
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215. .1528
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RIGIN
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BC011703

2088 bp mRNA linear PRI 02-AUG-2001
Homo sapiens, Similar to mosaic serine protease, clone MGC:19490
IMAGE:3610695, mRNA, complete cds.
BC011703
BC011703.1 GI:15079794
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1004 AAACTGGGCAGCTTCCCATCCCTGGCTGTGGCCAGATCATCATCATTGAATTCAACCCC
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TTCTCTGCCTGTTTCGACACTTCACAGAAGCTCTCGCTGAGACAGCCTGTAGGCAGATG
                                                   ValValGluileThrGluAsnSerGlnGluLeuArgMetArgAsnSerSerGlyProCys
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/protein_id="AAH11703.1"
/db_xref="G1:15079795"
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YQSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL"
                                                        Strausberg, R.

Strausberg, R.

Direct Submission

Submitted (30-JUL-2001) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

NIH-MGC Project URL: http://mgc.nci.nih.gov

Contact: MGC help desk

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing Center (NISC),

Gaithersburg, Maryland;

Web site: http://www.nisc.nih.gov/

Contact: http://www.nisc.nih.gov/
                                                                                                                                                                                                                                                                                                                     Web site:

'http://www.nisc.nih.gov/
Contact:

nisc_mgc@nbgri.nih.gov
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,
Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
Zhang,L.-H. and Green,B.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clone distribution: MGC clone distribution information can be four through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 27 Row: f Column: 19
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 8347148.
Location/Qualifiers
                  Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pglnProLeuAsnSerLeuAspValLysProLeuArgLysProArg
1. .2088
/organism="Homo sapiens"
/wol_type="mRNA"
/db_xref="taxon:9606"
/clone="MGC:19490 IMAGE:3610695"
/tissue type="Pancreas, adenocarcinoma"
/clone_Tib="NIH_MGC_39"
/lab_host="DH10E-R"
/note="Vector: pOTB7"
/codon_start=1
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Madison, E.L., Ong, E.O. and Yeh, J.C.

Nucleic acid molecules encoding transmembrane serine proteases, the encoded proteins and methods based thereon Patent: WO 0157194-A 71 09-AUG-2001; CORVAS INTERNATIONAL, INC. (US)

Location/Qualifiers
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CCGTGTGGTGGGTGGGAGGAGGCCTCTGTGGATTCTTGGCCTTGGCAGGTCAGCATCCA 876
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Sequence 71 from Patent WO0157194.
AX207967
AX207967.1 GI:15422563
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/db_xref="GI:15422564"
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SILDPHWVLTAAHCFRKHTDVFNWKVRAGSDKLGSFPSLAVAKIIIIBFNPMYPKDND
IALMKLQFPLTFSGTVRPICLPFFDEELTPATPLWIIGWGFTKQNGGKMSDILLQASV
QVIDSTRCNADDAYGGEVTEKMMCAGIPEGGVDTCQGDSGGPLMYQSDQWHVVGIVSW
GYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL"

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Smeekens, S.S., Lorimer, D.D., Wang, E., Hou, J. and Linnevers, C.
Direct Submission
Submitted (14-DEC-1999) Axys Pharmaceuticals, Inc, 180 Kimball Way,
South San Francisco, CA 94080, USA
Location/Qualifiers
1. 2079
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//mol type="mRNA"
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//db xref="taxon:9606"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2079)
Smeekens, S.S., Lorimer, D.D., Wang, E., Hou, J. and Linnevers, C.
MT-SP2, a novel type II membrane serine protease expressed in trachea, colon, and small intestine: identification, cloning, and chromosomal localization
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Homo sapiens type II membrane serine protease mRNA, complete cds.
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Madison, E.L., Ong, E.O. and Yeh, J.C.
Nucleic acid molecules encoding transmembrane serine proteases, encoded proteins and methods based thereon
Patent: WO 0157194-A 3 09-AUG-2001;
CORVAS INTERNATIONAL, INC. (US)
Location/Qualifiers
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62 CVs( 399 TGC( 82 Pro) 459 CCC 102 Val 122 Phe 519 GTC 519 TTC	44 6 6 2 V 6 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	202 Arg	262 Lys 984 AAJ 282 Met 1044 AT 302 G1 1104 GG	342 LeuC 1224 CTGC 362 GlyC 1284 GGGC 382 GlnC 1344 CAGC 402 Vals 402 Vals

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Gurney,A.L., Pan,J., Smith,V., Watanabe,C.K., Wood,W.I. and
422 AlaTyrLeuAsnTrpIleTyrAsnValTrpLysAlaGluLeu 435
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Genentech, Inc. (US)
Location/Qualifiers
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Sequence 329 from Patent WO0168848.
AX376262
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Eaton,D.L., Gao,W.Q., Pan,J., Botstein,D., Fong,S., Goddard,A.,
Godowski,P.J., Gurney,A.L., Smith,V., Tumas,D., Wood,W.I.,
Grimaldi,C.J., Hillan,K.J., Paoni,N.F., Roy,M.A. and Watanabe,C.K.
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Location/Qualifiers

1. 1793

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/clone="IMAGE:3623466"
/lab_host="Dancreas, adenocarcinoma"
/note="Vector: poTB7"
<1. 1219
                                                                                                                                                                                                                              BC012752 1793 bp mRNA linear PRI 20-AUG-2001
Homo sapiens, Similar to transmembrane protease, serine 4, clone
IMAGE:3623466, mRNA, partial cds.
BC012752
BC012752.1 GI:15215322
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Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                        Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1793)
Strausberg,R.
Direct Submission
Submitted (15-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
              /GlyProLeuMetTyrGlnSerAspGlnTrpHisValValGlyIle
                                                                          VSA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford,
Greene, Mark Ketteman and Anuradha Madan
                                                                                                                                                        3ATCTACAATGTCTGGAAGGCTGAGCTG 1505
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331 ATCATCATCATGAATTCAACCCCATGTACCCCAAAGACAATGACATGGCCCTCATGAAG
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                                                                                      IleIleIleAlaLeuLeuSerLeuAlaSerIleIleIleValValValLeuIleLysVal
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Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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92.53%
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д	971	TGCAATGCAGACGATGCGTACCAGGGGGAAGTCACCGAGAAGATGATGTGTGCAGGCATC 1030
>-	374	374 ProGluGlyGlyValAspThrCysGlnGlyAspSerGlyGlyProLeuMetTyrGlnSer 393
q	1031	1031 CCGGAAGGGGGTGTGGGACACCTGCCAGGTGACAGTGGGGCCCCTGATGTACCAATCT 1090
<b>&gt;</b>	394	AspGlnTrpHisValValGlyIleValSerTrpGlyTyrGlyClyGlyGlyDroSerThr 413
д	1001	1091 GACCAGGGCATGTGGGGGGCATCGTTAGCTGGGCTATGGCTGCGGGGGGCCCGAGCACC 1150
⋋	414	414 ProGlyValTyrThrLysValSerAlaTyrLeuAsnTrplleTyrAsnValTrpLysAla 433
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earch completed: November 23, 2003, 10:39:57 ob time : 5540.45 secs

1, Appli 2, Appli 2, Appli 24, Appl 9, Appli 25, Appl

Sequence Sequence

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Sequence Sequence 1, Appli 1, Appli 18, Appl 30, Appl 431, App 8, Appli 2, Appli

Sequence Sequence

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1, Appli
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APPLICANT: Bandman, Olga
Hillman, Jennifer L.
Yue, Henry
Guegler, Karl J.
Corley, Neil C.
Tang, Tom Y.
Shah, Purvi
TITLE OF INVENTION: HUMAN PROTEASE MOLECULES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/008,271A
FILING DATE: 16-Jan-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Incyte Pharmaceuticals, Inc
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
US-09-820-002-1
US-09-000-846-1
US-09-370-838-80
US-08-508-448C-15
US-09-370-838-79
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ATTORNEY/AGENT INFORMATION:
NAME: Mohan-Peterson, Sheela
REGISTRATION NUMBER: 41,201
REFERENCE/DOCKET NUMBER: PF-0458 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 18, Application US/09008271A Patent No. 6203979 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94304
COMPUTER READABLE FORM:
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Sequence 3, Appli
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Sequence 18, Appli
Sequence 188, Appli
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Sequence 3, Appli
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Sequence 1, Appli
                                                                                                                           ; Search time 87.359 Seconds (without alignments) 2197,846 Million cell updates/sec
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                                                                                            frame_plus_p2n model
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US-09-656-002-1
US-09-342-749-29
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Maximum Match 100%
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COMPOSITIONS, AND
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                                                                                                           1100 TCAGGCACACTCTGTCTGTCTTCTTTGATGAGGAGCTCACTCCAGCCACC
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Sequence 1. Application US/09656002

Patent No. 645568

GRIERAL INFORMATION:

APPLICANT: Mack, David

APPLICANT: Milson, Keith

TITLE OF INVENTION: OF SCREENING FOR COLORECTAL CANCER, COMP

TITLE OF INVENTION: OF SCREENING FOR COLORECTAL CANCER MODULATORS

TITLE OF INVENTION: OF SCREENING FOR COLORECTAL CANCER MODULATORS

FILE REFERENCE: A-69108/DJJD/AMS

CURRENT APPLICATION NUMBER: US 09/656,002

CURRENT FILING DATE: 2000-03-15

PRIOR APPLICATION NUMBER: US 09/493,444

PRIOR APPLICATION NUMBER: PCT/US 00/07044

PRIOR FILING DATE: 2000-03-15

NUMBER OF SEQ ID NOS: 3

SOFTWARE: PATENTIN Version 3.0

SSOFTWARE: PATENTIN Version 3.0

TYPE: DNA

CORGANISM: Home sapiens

US-09-656-002-1
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      TELEPHONE: 650-855-0555
TELEPHONE: 650-845-4166
INFORMATION SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 2038 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: COLNNOT13
CLONE: 1337018
SEQUENCE DESCRIPTION: SEQ ID NO
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US-09-342-749-29
is Sequence 29, Application US/09342749
j Patent No. 6166194
j GENERAL INFORMATION:
APPLICANT: Wong, Alexander K.C.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Teng, DAvid H.-F.
ITILE OF INVENTION: TMPRSS2 is a Tumor Suppressor
FILE REFERENCE: 2318-202
CURRENT APPLICATION NUMBER: US/09/342,749
CURRENT FILING DATE: 1999-06-29
BARLIER FILING DATE: 1998-06-29
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 29
LIGHT: 2479
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Matches:
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; ORGANISM: Homo sapiens
US-09-342-749-29
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Patent No. 6444419

GENERAL INFORMATION:

APPLICANT: Wong, Alexander K.C.

APPLICANT: Tavtigian, Sean V.

APPLICANT: Teng, David H.-F.

APPLICANT: Myriad Genetics, Inc.

TITLE OF INVENTION: TMPRSS2 is a Tumor Suppressor

FILE REFERENCE: 2318-202

CURRENT APPLICATION NUMBER: US/09/691,840

CURRENT FILING DATE: 2000-10-18

PRIOR APPLICATION NUMBER: US/09/342,749
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PRIOR FILING DATE: 1999-06-29;
PRIOR APPLICATION NUMBER: US 60;
PRIOR FILING DATE: 1998-06-29;
NUMBER OF SEQ ID NOS: 33;
SOFTWARE: Patentin Ver. 2.0;
SEQ ID NO 29;
LENGTH: 2479
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S-09-342-749-1
Sequence 1, Application US/093
Patent No. 6166194
GENERAL INFORMATION:
APPLICANT: Wong, Alexander K. APPLICANT: Tavigian, Sean V. APPLICANT: Tavigian, Sean V. APPLICANT: Teng, David H.-F. APPLICANT: Myriad Genetics, ITTLE OF INVENTION: TMPRSS2 iFILE REFERENCE: 2318-202
CURRENT FILING DATE: 1999-06-BARLIER FILING DATE: 1999-06-BARLIER FILING DATE: 1998-06-NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 1479
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
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NAME/KEY: conflict
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NAME/KEY: conflict
LOCATION: (985)
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APPLICANT: Wong, Alexander K.C.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Teng, David H.-F.
TITLE OF INVENTION: TMPRSS2 is a Tumor Suppressor FILE REFERENCE: 2318-202
CURRENT APPLICATION NUMBER: US/09/691,840
CURRENT FILING DATE: 2000-10-18
PRIOR APPLICATION NUMBER: US/09/342,749
PRIOR FILING DATE: 1999-06-29
PRIOR FILING DATE: 1998-06-29
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
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JS-09-691-840-1
Sequence 1, Application Ut
Patent No. 6444419
GENERAL INFORMATION:
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ORGANISM: Homo s
FEATURE:
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Sequence 1, Application US/09518046

Patent No. 6294663

GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
APPLICANT: Underwood, Lowell J.
TITLE OF INVENTION: Transmembrane Serine Protease Overexpressed
TITLE OF INVENTION: in Ovarian Carcinoma and Uses Thereof
FILE REFERENCE: D6192CIP
CURRENT APPLICATION NUMBER: US/09/518,046

CURRENT FILING DATE: 2000-03-02

EARLIER APPLICATION NUMBER: 09/261,416

EARLIER FILING DATE: 1999-03-03
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US-09-518-046-1
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APPLICANT: O'Brien, Timothy J.
APPLICANT: Underwood, Lowell J.
TITLE OF INVENTION: Transmembrane Serine Protitue OF INVENTION: In Ovarian Carcinoma and FILE REFERENCE: D6192CIP
CURRENT APPLICATION NUMBER: US/09/518,046
CURRENT FILING DATE: 2000-03-02
EARLIER APPLICATION NUMBER: 09/261,416
EARLIER FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 153
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S-09-518-046-3
Sequence 3, Application US/
Patent No. 6294663
GENERAL INFORMATION:
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LENGTH: 2544
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                                     353 ArgCysAsnAlaAspAspAlaTyrGlnGlyGluValThrGluLysMetMetCysAlaGly
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Sequence 1, Application US/09261416A
Patent No. 6291663
GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
APPLICANT: Underwood, Lowell J.
TITLE OF INVENTION: TADG-12: A No. 6291663el
TITLE OF INVENTION: Overexpressed in Ovarian
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CURRENT APPLICATION NUMBER:
CURRENT FILING DATE: 1999-03
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 1
LENGTH: 2416
TYPE: DNA
ORGANISM: Homo sapiens
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OTHER INFORMATION: C
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                       Sequence 188, Application US/09510738A
Patent NO. 6268165
GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
TITLE OF INVENTION: Compositions and Method
TITLE OF INVENTION: Ovarian Cancer
FILE REFERENCE: D6223CIP-A
CURRENT APPLICATION NUMBER: US/09/510,738A
CURRENT FILING DATE: 09/039,211
PRIOR FILING DATE: 03-14-1998
NUMBER OF SEQ ID NOS: 188
SEQ ID NO 188
LENGTH: 1783
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S-09-510-738A-188
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Patent No. 6518028

GENERAL INFORMATION:

APPLICANT: O'Brien, Timothy J.

TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of TITLE OF INVENTION: Ovarian Cancer

FILE REFERENCE: D6223CIP-A/Div

CURRENT APPLICATION NUMBER: US/09/861,966

CURRENT FILING DATE: 2001-05-21

PRIOR FILING DATE: 2000-02-22

NUMBER OF SEQ ID NOS: 188

SEQ ID NO 188

LENGTH: 1783
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US-09-861-966-188
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         1783
140
60
161
83
                                                                                                                                                                                         TGGGCCATTGTGGCTGTTCTCCTCAGG
          Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                 09-861-966-188 (1-1783)
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         1.36e-
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516 GAGGAGATGGGCTTC
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                               ercent Similarity:
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ignment Scores ed. No.:
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CICICCAGICCCCIGCCCTCACAGAAIACAICCAGCCIGIGIGCCICCCAGCIGCGGGC 1091
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                                      GluGluLeuThrProAlaThrProLeuTrpIleIleGlyTrpGlyPheThrLysGlnAsn
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CAGGCCCTGGTGGATGGCAAGATCTGTACCGTGACGGGCTGGGGCAACACG----CAGTAC
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TGCAATGGGGCTGACTTCTATGGAAACCAGATCAAGCCCCAAGATGTTCTGTGCTGGGCTAC
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                                                                                                         GlyGlyLysMetSerAspIleLeuGlnAlaSerValGlnValIleAspSerThrArg
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; Batent No. 6423543
; GENERAL INFORMATION:
; APPLICANT: Patrick Allen Marcotte
; APPLICANT: Lex M. Cowsert
; TITLE OF INVENTION: ANTISENSE MODULATION OF HEPSIN EXPRESSION
; FILE REFERENCE: RTS-0090
; CURRENT APPLICATION NUMBER: US/09/742,703
; CURRENT FILING DATE: 2000-12-20
; NUMBER OF SEQ ID NOS: 49
; SEQ ID NO 3
; LENGTH: 2363
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Indels:
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Best Local Similarity:
Query Match:
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; NAME/KEY: CDS
; LOCATION: (826).
US-09-742-703-3
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Pred. No.:
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AND

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PROTEINS, ENCODING HUMAN PROTEASE PROTEINS,
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--GCGGGGACCCTGCTACTTCTGACAGCC
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Matches:
Conservative:
Mismatches:
Indels:
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Patent No. 6482630;
GENERAL INFORMATION:
APPLICANT: Gan, Weiniu
APPLICANT: Ye, Jane
APPLICANT: DiFrancesco, Valentina
APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PRO
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
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TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION NUMBER: US/09/820,002
CURRENT APPLICATION NUMBER: 2001-03-29
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1615
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; ORGANISM: HUMAN
US-09-820-002-1
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US-09-820-002-1
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                                                                              JeuserLysAspArgSerThrLeuGlnValLeuAspSerAlaThr 118
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  IG1yG1uAspG1uG1uHisCysValLysSerPheProG1uG1yPro
                                                                                                                                                    GlyAsnTrpPheSerAlaCysPheAspAsnPheThrGluAlaLeuAlaGluThrAlaCys
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                                                                                                                                                                                                                                                                                                  159 AspLeuAspValValGluIleThrGluAsn-----
    LeuAspCysProLet
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Query Match:
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ORGANISM: Mus
FEATURE:
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
LOCATION:
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Sequence 1, Application US/0
Patent No. 5981830
GENERAL INFORMATION:
APPLICANT: WU, QINGYU
APPLICANT: SADLER, JASPE
TITLE OF INVENTION: KNOC
TITLE OF INVENTION: DISR
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                            ValserileGlnTyr
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COMPUTER READABLE FORM:
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Matches:
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                                                                                          Version
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Versi
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/000,846
FILING DATE: 30-DEC-1997
CLASSIFICATION: 800
PRIOR APPLICATION: 800
PRIOR APPLICATION NUMBER: US 08/866,058
FILING DATE: 30-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: LEBOVITZ, RICHARD M.
REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: BERLX 65P1
TELEPHONE: 703-243-6333
TELEPHONE: 703-243-6410
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1605 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TYPE: MATEURAL DATA:
ATTORNEY INDEAR
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                                     uLysThrProArgValValGlyGlyGluGluAlaSerValAspSerTrpProTrpGlnVa
                                                     Sequence 80, Application US/09370838

Sequence 80, Application US/09370838

Patent No. 6444425

Patent No. 6444425

Patent No. 6444425

APPLICANT: Reed, Steven G.

APPLICANT: Lodes, Michael J.

APPLICANT: Mohamath, Roadoh

APPLICANT: Secrist, Heather

TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF

TITLE OF INVENTION: LUNG CANCER AND METHODS FOR THEIR USE

FILE REFERENCE: 210121.475c1

CURRENT APPLICATION NUMBER: US/09/370,838

CURRENT FILING DATE: 1999-08-09

BARLIER APPLICATION NUMBER: US 09/285,323

BARLIER FILING DATE: 1999-04-02

NUMBER OF SEQ ID NOS: 289

SOFTWARE: FASTSEQ for Windows Version 3.0
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1222 GGAGTGGATCTTCA
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258 AlaGlySerAspLysLeuGlySerPheProSerLeu----AlaValAlaLysIleIle 275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GluThrPheArgLysValGlyIleProlleIleIleAlaLeuLeuSerLeuAlaSerIle
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Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                             sapien
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Best Local Similarity:
Query Match:
DB:
; SEQ ID NO 80
; LENGTH: 1460
; TYPE: DNA
; ORGANISM: HOMO S
US-09-370-838-80
                                                                                                                                                                                                        Alignment Scores Pred. No.:
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1126 GGTGGAGTGGACGCATGTCAGGGTGACTCTGGTGGCCCACTAGTACAAGAAGACTCCACGG 1185
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                                                              316 LeuThrProAlaThrProLeuTrplleIleGlyTrpGlyPheThrLysGlnAsnGlyGly 335
                                                                                                                                                                                                                                                                                                                                 CysGlnGlyAspSerGlyGlyProLeuMetTyrGlnSerAspGln 395
                                                                                                     SerGlyThrValArgProlleCysLeuProPhePheAspGluGlu 315
                                                                                                                          336 LysMetSerAspileLeuGinAlaSerValGlnValileAspSerThrArgCysAsn 355
276 ilelleGluPheAsnProMetTyrProLysAspAsnAspIleAlaLeuMetLysLeuGln 295
                                                                                                                                                                                                                                                                                                                                                                                                 -----TrpHisValValGlyIleValSerTrpGlyTyrGlyCysGlyGlyProSerThr 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                          376 GlyGlyValAspThr
                                                                                                                                                                                  949 AFFCCACCTGGCTCT
                                                                                                                       889 AACAGTGTCACCTT
                                                                                                       296 PheProLeuThrPh
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                                                                                                                                                                                                                                                                                                                                                                                                                               1186 CGCCTTTGGTTTAT
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earch completed: November 23, 2003, 12:08:53 ob time : 126.359 secs

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Sequence 217, App Sequence 217, App Sequence 21, Appli Sequence 22, Appli Sequence 22, Appli Sequence 22, Appli Sequence 2, Appli Sequence 274, App Sequence 274, App Sequence 274, App Sequence 229, App Sequence 229, App Sequence 229, App Sequence 229, App Sequence 229, App Sequence 329, App Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yue, Henry
Guegler, Karl J.
Corley, Neil C.
Tang, Tom Y.
Shah, Purvi
TITLE OF INVENTION: HUMAN PROTEASE MOLECULES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
            RESULT 1
US-10-180-719-18
Sequence 18, Application US/10180719
Publication No. US20030166246A1
GENERAL INFORMATION:
Hillman, Jennifer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94304
COMPUTER READABLE FORM:

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      2
 RESULT 1
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MODBL=frame+ p2n.model -DEV=xlh

2=/cgn2 1/USPTO spool/US09607745/runat 21112003 144347_22270/app_query.fasta_1.1038

DB=Published Applications NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1

LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62

LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62

TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100

THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0

MAXLEN=2000000000 -USER=US09607745 @CGN 1 1 424 @runat 21112003 144347 22270

NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100

LONGLOG -DEV TIMEOÜT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5

FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 18, Appl
                                                                                                                                     ; Search time 467.909 Seconds (without alignments) 3038.343 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                   US-09-607-745-2
2342
1 MDPDSDQPLNSLDVKPLRKP.....VYTKVSAYLNWIYNVWKAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Published Applications NA:*

1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/DCT_NEW_PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*

4: /cgn2_6/ptodata/1/pubpna/USO6_PUBGOMB.seq:*

5: /cgn2_6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*

6: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*

7: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

8: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*

10: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*

11: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*

12: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*

13: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*

14: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*

15: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*

16: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*

17: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*

16: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*

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17: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
                       GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
                                                                                                   frame_plus_p2n model
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Matches:
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                                       PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/008,271
FILING DATE: 16-Jan-1998
ATTORNEY/AGENT INFORMATION:
NAME: Mohan-Peterson, Sheela
REGISTRATION NUMBER: 41,201
REFERENCE/DOCKET NUMBER: PF-0458 US
TELECOMMUNICATION INFORMATION:
TELEFAX: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
IENGTH: 2038 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
SOFTWARE: FastSEQ for Windows Ver:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/180,719
FILING DATE: 25-Jun-2002
PRIOR APPLICATION DATA:
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:ON: SEQ ID
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CLONE: 1337018
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US-09-851-588-7

Sequence 7, Application US/09851588

Patent No. US20020042067A1

GENERAL INFORMATION:

APPLICANT: Mack, David

APPLICANT: Wilson, Keith E.

TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSING COLORECTAL CANCER, COMI

TITLE OF INVENTION: OSCREENING FOR COLORECTAL CANCER MODULATORS

TITLE OF INVENTION: OSCREENING FOR COLORECTAL CANCER MODULATORS

TITLE OF INVENTION: OSCREENING FOR COLORECTAL CANCER MODULATORS

TITLE OF INVENTION: OSCREENING FOR COLORECTAL CANCER MODULATORS

TITLE OF INVENTION: OSCREENING FOR COLORECTAL CANCER MODULATORS

TITLE OF INVENTION NUMBER: US/09/851,588

CURRENT APPLICATION NUMBER: US 09/656,002

PRIOR FILING DATE: 2000-08-17

PRIOR FILING DATE: 2000-09-06

NUMBER OF SEQ ID NOS: 9

SOFTWARE: PatentIn Version 3.1

SEQ ID NO 7

LENGTH: 2081

TYPE: DNA
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321

1303

1363

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RESULT.

1 US-10-097-340-317

1 US-10-097-340-317

1 Sequence 317, Application US/10097340

2 Sequence 317, Application Worlson

2 Sequence 317, Application Worlson

2 Emblication No. US20030087250Al

3 Publication No. US20030087250Al

3 PUBLICANT: Manjula GANNAWARANU

3 APPLICANT: Shubhand; KANATKAR

4 APPLICANT: Shubhand; KANATKAR

4 APPLICANT: Rachel E. MEYERS

3 APPLICANT: Rece of COVATE

4 APPLICANT: Peter OLANT

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Matches:
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2337.00
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     ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (215)..(1528)
OTHER INFORMATION:
S-09-851-588-7
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Conservative:
Mismatches:
Indels:
Gaps:
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                       TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(2307)
OTHER INFORMATION: n = A
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SOFTWARE: FastSEQ
SEQ ID NO 317
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US-10-171-211-217

1 Sequence 217, Application US/10171311

2 Sequence 217, Application US/10171311

3 Publication No. US20030087270A1

5 Publication No. US20030087270A1

5 Publication No. US20030087270A1

5 APPLICANT: Schlegel, Robert

5 APPLICANT: Chen, Yan

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5 APPLICANT: Chen, Yan

5 APPLICANT: Chen, Yan

5 APPLICANT: Chen, Yan

5 APPLICANT: Chen, Yan

6 APPLICANT: Chenshaw, Manjula

5 APPLICANT: Glatt, Karen

6 APPLICANT: Glatt, Karen

7 TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR

7 TITLE OF INVENTION: DERTIFICATION, ASSESSMENT, PREVENTION, AND THER,

7 TITLE OF INVENTION: DERVICAL CANCER

7 TITLE OF INVENTION: UNMERR: US/10/171,311

7 CURRENT APPLICATION NUMBER: US 60/298,159

7 PRIOR FILING DATE: 2001-06-13

7 PRIOR FILING DATE: 2001-06-13

7 PRIOR FILING DATE: 2001-06-13

7 PRIOR FILING DATE: 2001-06-13

7 PRIOR FILING DATE: 2001-11-14

7 NUMBER OF SEQ ID NOS: 238

7 SEQ ID NO 217

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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: 1691, 1698, 1705, 1708, 1709, 1713, 1717, 1720,
LOCATION: 1733, 1741, 1746, 1748, 1755, 1770, 1774, 1791,
LOCATION: 1838, 1856, 1859, 1864, 1908, 1959, 1997, 2012,
OTHER INFORMATION: n = A,T,C or G
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; Publication No. US20030148295A1
; Publication No. US20030148295A1
; GENERAL INFORMATION:
; APPLICANT: WAN, JACKSON
; APPLICANT: WANG, YIXIN
; TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF
; FILE REFERENCE: 15117.0012
; CURRENT APPLICATION NUMBER: US/10/101,510
; CURRENT FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: 60/276,947
; PRIOR FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 805
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 634
; LENGTH: 2165
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-101-510-634
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US-09-851-588-5

i Sequence 5, Application US/09851588

i Patent No. US2020042067A1

i GENERAL INFORMATION:

APPLICANT: Mack, David

APPLICANT: Milson, Keith E.

TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSING COLORECTAL CANCER, COMP

TITLE OF INVENTION: OF SCREENING FOR COLORECTAL CANCER, COMP

TITLE OF INVENTION: OF SCREENING FOR COLORECTAL CANCER, COMP

TITLE OF INVENTION: OF SCREENING FOR COLORECTAL CANCER, COMP

TITLE OF INVENTION: OF SCREENING FOR COLORECTAL CANCER, COMP

TITLE OF INVENTION: OF SCREENING FOR COLORECTAL CANCER, COMP

TITLE OF INVENTION: OF SCREENING FOR COLORECTAL CANCER, COMP

CURRENT APPLICATION NUMBER: US 09/656,002

PRIOR APPLICATION NUMBER: US 09/656,002

PRIOR FILLING DATE: 2000-09-06

NUMBER OF SEQ ID NOS: 9

SOFTWARE: Patentin version 3.1

SOFTWARE: Patentin version 3.1

CREANISM: Homo sapiens

US-09-851-588-5
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S-09-776-191-71
Sequence 71, Application US/09776191
Publication No. US20030119168A1
GENERAL INFORMATION:
APPLICANT: Edwin L. Madison
APPLICANT: Edwin L. Madison
APPLICANT: Edwin L. Madison
APPLICANT: Corvas International, Inc.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING
TITLE OF INVENTION: METHODS BASED THEREON
FILE REFERENCE: 24745-1607
CURRENT APPLICATION NUMBER: 60/213,124
PRIOR FILING DATE: 2000-06-22
PRIOR FILING DATE: 2000-06-22
PRIOR FILING DATE: 2000-06-22
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PRIOR FILING DATE: 2000-02-03
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; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 71
; LENGTH: 2079
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (251)...(1522)
; OTHER INFORMATION: Nucleotide sequence encoding tra
; OTHER INFORMATION: Nucleotide sequence
; OTHER INFORMATION: Nucleotide sequence
; DATABASE ACCESSION NUMBER: GenBank NM016425
; DATABASE ENTRY DATE: 2000-11-06
US-09-776-191-71
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Matches:
Conservative:
Mismatches:
Indels:
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Mismatches:
Indels:
Gaps:
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; CTHER INFORMATION: CJA8 cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (251) ..(1522)
; OTHER INFORMATION: human CGA8
US-10-264-820-22
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Percent Similarity:
Best Local Similarity:
Query Match:
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S-10-264-820-22
Sequence 22, Application US/1026452.
Publication No. US20030108926A1
GENERAL INFORMATION:
APPLICANT: EDS Biotechnology, Inc.
TITLE OF INVENTION: No. US20030108926A1e1 Methods of DTITLE OF INVENTION: Compositions, and Methods of ScreTILE OF INVENTION: Compositions, and Methods of ScreTILE REFERENCE: 018501-0061410S
CURRENT APPLICATION NUMBER: US/10/264,820
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: US 09/268,866
PRIOR FILING DATE: 1999-03-15
PRIOR FILING DATE: 1999-11-09
PRIOR FILING DATE: 1999-11-09
PRIOR FILING DATE: 1999-11-29
PRIOR FILING DATE: 1999-11-29
PRIOR FILING DATE: 1999-11-29
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: US 09/453,850
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: US 09/453,850
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: US 09/453,444
PRIOR APPLICATION NUMBER: US 09/525,993
""TOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: US 09/525,993
""TOR FILING DATE: 2000-03-15
""TOR FILING DATE: 2000-03-15
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                                                                                    GlyGlyProLeuMetTyrGlnSerAspGlnTrpHisValValGlyIl
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S-09-776-191-3
Sequence 3, Application US/09776191
Publication No. US20030119168A1
GENERAL INFORMATION:
APPLICANT: Edwin L. Madison
APPLICANT: Giunn-Chern Yeh
APPLICANT: Jiunn-Chern Yeh
APPLICANT: Orvas International, Inc.
TITLE OF INVENTION: TRANSMEMBRANE SERINE PROTEASES, THITLE OF INVENTION: TRANSMEMBRANE SERINE PROTEASES, TITLE OF INVENTION: METHODS BASED THEREON
FILE REFERENCE: 24745-1607
CURRENT APPLICATION NUMBER: US/09/776,191
CURRENT APPLICATION NUMBER: 60/213,124
PRIOR APPLICATION NUMBER: 60/213,124
PRIOR FILING DATE: 2000-06-22
PRIOR FILING DATE: 2000-06-22
PRIOR FILING DATE: 2000-06-22
PRIOR FILING DATE: 2000-02-03
PRIOR FILING DATE: 2000-02-03
PRIOR FILING DATE: 2000-02-08
PRIOR FILING DATE: 2000-02-08
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 2137
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Publication No. US20030060612A1
GENERAL INFORMATION:
APPLICANT: Goddard, Audrey
APPLICANT: Goddwski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Polakis, Paul
APPLICANT: Smith, Victoria
APPLICANT: Swith, Victoria
APPLICANT: Wu, Thomas D.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
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CURRENT APPLICATION NUMBER: US/09/888,257A
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/063,540
PRIOR APPLICATION NUMBER: US 60/063,540
PRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-09-10
PRIOR FILING DATE: 1998-09-10
PRIOR FILING DATE: 1998-09-10
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: US 60/103,678
PRIOR APPLICATION NUMBER: US 60/235,451
PRIOR FILING DATE: 1999-06-02
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: 1999-09-01
PRIOR FILING DATE: 1999-09-01
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OR APPLICATION NUMBER: 60/099812
OR PILING DATE: 1998-09-10
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Publication No. US20030073129A1
GENERAL INPORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Bestein, David
APPLICANT: Bestein, David
APPLICANT: Bestein, David
APPLICANT: Bestein, David
APPLICANT: Gaco, Wel-Chiang
APPLICANT: Gaco, Wel-Chiang
APPLICANT: Gadard, Audrey
APPLICANT: Galandi, Christopher J.
APPLICANT: Galandi, Christopher J.
APPLICANT: Galandi, Christopher J.
APPLICANT: Garney, Austin L.
APPLICANT: Garney, Austin L.
APPLICANT: Brinaldi, Christopher J.
APPLICANT: Brinaldi, Christopher J.
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APPLICANT: Brinaldi, Christopher J.
APPLICANT: Stewart, Timothy A.
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APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, 1909-09-01
CURRENT FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098750
PRIOR FILING DATE: 1998-09-01
PRIOR FILING DATE: 1998-09-01
PRIOR PLING DATE: 1998-09-02
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PRIOR PLING DATE: 1998-09-03
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δ	182	LeuSerG1	VSerLeuValSerI	euHisCysLeuAlaCy	CLeuLysThrPro	201
엄	744	-65	creecheereree	recacrercriectro	creadacccc	
λõ	202	ArgValVa]	GlyGlyGluGlu <sup>2</sup> 	ValGlyGlyGluGluAlaSerValAspSerTrpProTrpGlr	ValSerIleGln	
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λõ	222	TyrAspLys	spLysGlnHisValCysG	sGlyGlySerIleLeuAspProHisTrpVa	lleuThrAla	241
업	864	TACGACAA	Acadcacercrere	GAGGGAGCATCCTGG	ccrcaceca	923
λõ	242	AlaHisCys	sCysPheArgLysHisThrAspValPho	hrAspValPheAsnTr	heAsnTrpLysValArgAlaGlySerAsp	261
අුග	924	-8 -8	CTTCAGGAAACATZ	CCGATGTTCAACTC	GCAGGCTCAGAC	983
δ	262	LysLeuGly	VSerPheProSerI	SerLeuAlaValAlaLysIle	llellelleGluPheAsnPro	281
අධ	984	AAACTGGGC	TGGGCAGCTTCCCATCC	TGGCTGTGGCCAAGAT	ATCATCATTGAATTCAACCCC	1043
<i>\</i> 0	282	et 7	JLYSASPASDASPI	IleAlaLeuMetLysLe	InPheProLeuThrPheSer	301
qa	1044	ATGTACCC	CAAAGACAATGACA	TCGCCCTCATGAAGCTGC	AGTTCCCACTCACTTTCTCA	1103
λŏ	302	GlyThrva]	lArgProlleCysI	euProPhePheAspG1	roAlaThrPro	321
qa	1104	GGCACAGT	CAGGCCCATCTGTC	TGCCCTTCTTGATGA		1163
š	322	LeuTrplle	elleglyTrpGlyF	heThrLysGlnAsnGl	LeuTrplleIleGlyTrpGlyPheThrLysGlnAsnGlyGlyLysMetSerAsplleLeu	341
qq	1164	CTCTGGATC	CATTGGATGGGGCT	TTACGAAGCAGAATGG	_rh	1223

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Sequence 274, Application US/10015387A
Publication No. US20030135034A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Eaton, Dan 1.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Fong, Sherman
APPLICANT: Goodward, Audrey
APPLICANT: Goodward, Austin L.
APPLICANT: Goodward, Austin L.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Aponi, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane PolyTITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2830P1C54
CURRENT FILING DATE: 2001-12-12
Prior Application removed - See File Wrapper or Parknament application removed - See File LENGTH APPLICATION NUMBER: LENGTH APPLICATION NUMBER: LENGTH APPLICATION NUMBER: LENGTH APPLICATION NUMBER: LENGTH APPLICATION NUMBER: LENGTH APPLICATION NUMBER: LENGTH APPLICATION NUMBER: LENGTH APPLICATION LENGTH APPLICATION LENGTH APPLICATION LENGTH APPLICATION LENGTH APPLICATION LENGTH APPLICATION LENGTH APPLICATION LENGTH APPLICATION LENGTH APPLICATION LENGTH APPLICATION LENGTH APPLICATION LENGTH APPLICATION LENGTH APPLICATION LENGTH APPLICATION LENGTH APPLICATION LENGTH APPLICATION LENGTH APPLICATION LENGTH APPLICATION LENGTH APPLICATION LENGTH APPLICATION LENGTH APPLICATION LENGTH APPLICATION LENGTH APPLICATION LENGTH APPLICATION LENGTH APPLICATION LENGTH APPLICATION LENGTH APPLICATION LENGTH APPLICATION LENGTH APPLICATION LENGTH APPLICATION LENGTH APPLICATION LENGTH APPLICATION LENGTH APPLICATION LENGTH APPLICATION LENGTH APPLICATION LENGTH APPLICATION LENGTH APPLICATION LENGTH APPLICATION LENGTH APPLICATION LENGTH APPLICATION LENGTH APPLICATION LENGTH APPLICATION LENGTH APPLICATION LENGTH APPLICATION LENGTH APPLICATION LENGTH APPLICATION LENGTH APPLICATION LENGTH APPLICATION LENGTH APPLICATION LENGTH APPLICATION LENGTH APPLICATION LENGTH APPLICATION LENGTH APPLICATION LENGTH APPLICATION LENGTH APPLICATION LENGTH APPLICATION LENGTH APPLICATION LENGTH APPLICATION LENGTH APPLICA
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 ValValGluIleThrGluAsnSerGlnGluLeuArgMetArgAsnSerSerGlyProCys
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APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Eaton, Dan 1.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Godwski, Paul J.
APPLICANT: Godwski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
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                              Sequence 111, Application US/10063735
Sequence 111, Application US/10063735
Publication No. US20030138882A1
GENERAL INFORMATION:
APPLICANT: Eaton, Dan L.
APPLICANT: Gerritsen, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Godwski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Wood, William L.
APPLICANT: Wood, William L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3230R1C1
CURRENT APPLICATION NUMBER: US/10/063,735
CURRENT FILING DATE: 2002-05-08
Prior Application removed - See Palm or File Wrapper NUMBER OF SEQ ID NOS: 170
SEQ ID NO 111
LENGTH: 2063
TYPE: NAA
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Conservative:
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ORGANISM: Homo
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APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Pani, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Pol
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2830P1C7
CURRENT APPLICATION NUMBER: US/10/006,130A
CURRENT FILING DATE: 2002-03-19
Prior Application removed - See File Wrapper or Pa
NUMBER OF SEQ ID NOS: 477
SEQ ID NO 274
LENGTH: 2063
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2003, November 3

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GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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using frame\_plus\_p2n model search nucleic ı 1 protein 07:53:00 ; Search time 3092.27 Seconds (without alignments) 3418.993 Million cell updates/sec 435 .....VYTKVSAYLNWIYNVWKAEL US-09-607-745-2 2342 1 MDPDSDQPLNSLDVKPLRKP. 2003, November 23 .tle: :rfect score: squence: on: ដ

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NUTS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
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## SUMMARIES

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## ALIGNMENTS

HTC 12-JUL-2001 Homo sapiens (human) Homo sapiens Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. 1 (bases 1 to 1973) clone BC004855
Homo sapiens, Similar to transmembrane protease, serine 4, IMAGE:3835263, mRNA.
BC004855
BC004855.1 GI:14709533 ACCESSION VERSION KEYWORDS SOURCE ORGANISM RESULT 1 BC004855 LOCUS DEFINITION REFERENCE

160

722

180

782

200

220 902 240 962 260

-09-607-745-2.rs

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AK078890

Mus musculus adult male colon cDNA, RIKEN full-length enriched library, clone:9030622G02 product:SIMILAR TO TRANSMEMBRANE PROTEASE, SERINE 4 homolog [Mus musculus], full insert sequence.
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                                                                   SerglyThrValArgProlleCysLeuProPhePheAspGluGluLeuThrProAlaThr
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HTC; CAP trapper.

Mus musculus (house mouse)

Mus musculus
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 8347148
This clone has the following problem: frame shifted.

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Strausberg, R.

Direct Submission

Submitted (21-MAR-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia
Greene, Mark Ketteman and Anuradha Madan
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NELECTION OF A. Mattaker, C., Wilming, L., Functional annotation of a full-length mouse cDNA collection Nature 409 (6821), 685-690 (2001)

NELECTION OF A. Mattaker, C., Milming, L., Functional annotation of a full-length mouse cDNA collection Nature 409 (6821), 685-690 (2001)
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The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

E G (bases 1 to 217)

Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nishi,K., Nomura,K., Numazaki,A., Murata,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
                                                                                                                                                                                                                                                                            Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
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       Craniata, Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
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• full-length cDNA cloning
303, 19-44 (1999)
       Chordata;
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Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/.
URL:http://fantom.gsc.riken.go.jp/.
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[Mus musculus] (SPTR|AAH21368, evidence: FASTY, 92%ID,
100%length, match=1201)
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
/o. - 1722
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/strain="C57BL/6J"
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us-09-607-745-2.rst

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi Mammalia; Butheria, Primates; Catarrhini; Hominidae, Homo.

E 1 (bases 1 to 844)

S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATC

cDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM266 row: d column: 18

High quality sequence stop: 712.
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Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Musinae;

Mammaliai; Butheria; Rodentia; Sciurognathi; Muridae; Musinae;

Mational Institutes of Health, Mammalian Gene Collection (MGC)

Mational Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished

Contact: Robert Strausberg, Ph.D.

Bmail: Capaba-rômail.inh.gov

Tissue procurement: The Cepko Laboratory

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium

CLONA Library Agencourt Bioscience Corporation

Clone distribution: MGC Clone distribution information can be http://image.llnl.gov

Plate: LibMuil129 row: i column: 06

High quality sequence stop: 665.

Loganism="Mus musculus"

/ mol type="makna"

/ strain="RyBN"

/ clone="MacBE:652442"

/ lab host=PHHOB (TI phage-resistant)"

/ lab host=PHHOB (TI phage-resistant)"

/ lob host=PHHOB (TI phage-resistant)"

/ clone Lib="Mul Colon; Vector: pCMV-SPORT6; Site_I: NotI;

Site_I: SalI; Cloned unidirectionally. Primer: Oligo dT.
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                                                                421 CCCTGTCTCTCAGGCTCCCTGGTCTCCTGCAGTCTTGCCTGTGGGAAGAGCCTGAAG
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                                                                                                                                                                                   ATCCAGTACGACAAACAGCACGTCTGTGGAGGAGCATCCTGGGACCCCCCACTGGGTCCTC
                                                                                                                         ACCCCCCGTGTGGTGGGTGGGGAGGCCTCTGTGGATTCTTGGCCTTGGCAGGTCAGC
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AGENCOURT 1015816
IMAGE:6529422 5',
BU522841
BU522841.1 GI:22
EST.
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                                              ProCysLeuSerG
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Matches:
Conservative:
Mismatches:
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BE616663 920 bp mRNA linear EST 24-AUG-2000 601278696F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3610990 5', mRNA sequence.
BE616663
BE616663.1 GI:9898262
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/clone="IMAGE:3610990"
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Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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E 1 (bases 1 to 920)

S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM267 row: o column: 23

High quality sequence start: 5

High quality sequence start: 5

High quality sequence stop: 819.
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                                                                                             LeuThrProAlaThrProLeuTrpIleIleGlyTrpGlyPheThrLysGlnAsnGlyGly
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Site_2: Not1; The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was adjusted to have about 60nt. The cDNA vector. An RNA strand converted to a DNA strand by Okapama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."
                                                                           BM795149 617 bp mRNA linear EST 05-MAR-2002
K-EST0076707 S21SNU520 Homo sapiens cDNA clone S21SNU520-27-H07 5',
mRNA sequence.
                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 617)

Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.

21C Frontier Korean EST Project 2001

Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                        Contact: Kim YS
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eceun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 27 row: H column: 07
High quality sequence stop: 617.
Location/Qualifiers
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Matches:
Conservative:
Mismatches:
Indels:
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902
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                                                 TCGGCCACAGGGAACTGGTTCTCTGCCTGTTTCGACAACTTCACAGAAGCTCTCGCTGAG
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                                                                                                                                                                                  erIleGlnTyrAspLysGlnHisValCysGlyGlySerIleLeuAsp
                     62 GAAGGGCCTGCAGTGGCAGTCCGCCTCTCCCAAGGACCGATCCACACGCAGGGGGCTGCTGGAC
                                                                                                ProAspGlnAspLeuAspValValGluIleThrGluAsnSerGlnGluLeuArgMetArg
                                                                                                        242 CCAGACCAGGATCTGGATGTTGTAAAAAAAAAAAAAAGCAGGAGCTTCGCATGCGG
                                                                                                                                                               362 AAGAGCCTGAAGACCCCCCGTGTGGTGGNGTGGGGAAGGANGCCCTCTGTGGATTCTTGG
GACGGAGAGCTGGACTGTCCCTTGGGGGAGGACGAGGAGCACTGTGTCAAGAGCTTCCCC
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87 NCI_CGAP_Co24
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GCAGCCACAGGGACCTGGGCCTCAGTCTTCGACAACTTCACAGAAGCACTGGCCAAG
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/db_xref="taxon:10090"
/clone="IMAGE:6529864"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_Co24"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: Not
Site_2: Sall; Cloned unidirectionally. Primer: Oligc
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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ON UI-E-CR0-adk-g-09-0-UI.rl UI-B-CR0 Homo sapiens cDNA clone
UI-E-CR0-adk-g-09-0-UI.rl UI-B-CR0 Homo sapiens cDNA clone
UI-E-CR0-adk-g-09-0-UI 5', mRNA sequence.

BM686292

BM686292.1 GI:18999550

EST.

Homo sapiens (human)

SM Homo sapiens (human)

SM Homo sapiens (human)

Homo sapiens (human)

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SM Homo sapiens (human)

Nammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

SM Homo sapiens (human)

Normalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

SM Normalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

SM Normalization and subtraction: two approaches to facilitate gene
354 s-AsnAlaAspAspAlaTyr---GlnGlyGluValThrGluLysMetMetCysAlaGlyI
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|GCCTACCCAAGGGGAAGGGACCCGCTGAAATGGTGGGGGGACAGG
                                           ydlyvalaspihr---CysGlnGlyAspSer---GlyGlyProLeuM
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BG822914 804 bp mRNA linear EST 22-MAY-2001 602727917F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4867108 5', mRNA sequence.
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Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 804)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                           ArgMetArgAsnSerSerGlyProCysLeuSerGlySer-LeuValSer
Length:
Matches:
Conservative:
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us-09-607-745-2.rs

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1. .804
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| /mol_type="mRNA"
| /db_xref="taxon:9606"
| /clone="IMAGE:4867108"
| /tissue_type="adenocarcinoma cell line"
| /lab_host="DH10B (phage-resistant)"
| /clone lib="NIH MGC 15"
| /clone lib="NIH MGC 15"
| /clone lib="Organ: colon; Vector: pOTB7; Site 1: Xhol; Site 2: EcoR1; colon; Vector: pOTB7; Site 1: Xhol; Site 2: EcoR1; colon Vector: potming. Directionally cloned into EcoR1/Xhol sites using the following 5; adaptor: GGCACGAGG(G). Site-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)"
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DNA Sequencing by: NIH Intramural Sequencing Center Clone distribution: MGC clone distribution information found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLCM1735 row: b column: 05
High quality sequence stop: 793.
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Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
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Contact: Robert Strausberg, Ph.D.
Condact: Robert Strausberg, Ph.D.
Condact: Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: NIH Intramural Sequencing Center
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
Location/Qualifiers
High quality sequence stop: 763.
High quality sequence stop: 763.

Location/Qualifiers
I. .1007

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/ clone lib="NHH MGC 15"
/ clone dinto EccRI/KhoI sites using the following 5, adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1 sake. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)"

NT 240 a 291 c 293 g 183 t
                                                                                                       BG386903 1007 bp mRNA linear BST 12-MAR-2001 602454702F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4582969 5', mRNA sequence.
BG386903 GI:13280452
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1 (bases 1 to 1007)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Mus musculus (house mouse)

Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mu

El (bases 1 to 920)

S NIH-MGC http://mgc.nci.nih.gov/.

In (bases 1 to 920)

L Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: The Cepko Laboratory

CONA Library Preparation: Life Technologies, Inc.

CONA Library Preparation: Life Technologies, Inc.

CONA Library Arrayed by: The I.M.A.G.B. Consortium

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAMA13891 row: f column: 06

High quality sequence stop: 599.

Location/Qualifiers

1. 920

/organism="Mus musculus"
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/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:6395909"
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                                                            TGTCCCTTGGGGGAGGACGAGGAGCACTGTGTCAAGAGCTTCCCCGAAGGGCCTGCAGTG
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IMAGE:6395909 5', mRNA sequence.
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/lab_host="DH10B (TI phage-resistant)"
/clone_lib="NCI_CGAP_Co24"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI
Site_2: SalI; Cloned unidirectionally. Primer: Oligo
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP_Library."
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Eukaryotta; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Musmaalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Musc.

In Dases 1 to 689)

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

In Unpublished
Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Location/Qualifiers

In G899

| Norganism="Musculus" |
| Norganism="Musculus" |
| Norganism="Musculus" |
| Norganism="Musculus" |
| Note="Taxon:10090" |
| Note="Tone" "InhAE: 4989048" |
| Note="Tone" "InhAE: 4989048" |
| Note="Tone" unidirectionally Primer: Oligo dT.
| Average insert size 1.6 kb. Constructed by Life |
| Technologies. Note: this is a NCI_CGAP Library." |
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                                                                            689 bp mRNA linear EST 12-JUN-2001 CGAP_Co24 Mus musculus cDNA clone IMAGE:4989048 5',
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BG966811
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Mus musculus (house mouse)
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Homo saplens

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases I to 879)

Mational Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:

Location/Colone distribution: MGC Clone distribution information can be http://image.llni.gov

Plate: LLCWA67 row: c column: 16

High quality sequence stop: 733.

Location/Qualifiers

I. 879

// Organism="MROM"

// Ab xref="Taxon:9606"

// Clone="MAGE:3610695"

// Lissue-Lype="adenocarcinoma"

// Lab host="MHAGE:3610695"

// Lissue-Lype="adenocarcinoma"

// Lissue-Lype="adenocarcinoma"

// Lab host="MHAGE:3610695"

// Lissue-Lype="adenocarcinoma"

// Lab host="MHAGE:3610695"

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BE616186.1 GI:9897785
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CB142902

CB142902.1 GI:28119586

EST.

Homo sapiens (human)

Momo sapiens (human)

Romo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 515)

S Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
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## ALIGNMENTS

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Protease D-G cataytic domain fusion gene construct amino acid sequence
                                                                                                                                                                 Serine protease; D-G; human; zymogen; enzyme; cytostatic; antiinflammatory; dermatological; anticoagulation; cancer; skin disorder; neuropathic pain; inflammatory disorder; coagulation diathesis; thrombosis; laundry detergent; skin care;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     60..284
/note= "Protease D-G catalytic domain"
                                                                                                                                                                                                                                                                                                                                                                 ...27
|Tabel= Prolactin_signal_sequence
                                                                                                                                                                                                                                                                                                                                                                                                        28..292
/label= Mature_protease_D-G
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                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
AAG78578 standard; Protein; 292 AA
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/note= "6xHIS-TAG"
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(first entry)

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08-JUN-2001; 2001WO-US18568
           30-JUN-2000; 2000US-06
                (ORTH ) ORTHO-MCNEIL F
                           WPI; 2002-106601/14.
N-PSDB; AAI64290.
                      Qi J,
10-JAN-2002
                      Darrow AL,
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lrade-Gordon

And

HARM INC

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a serine protease called D-G protein which is modulators that are useful for treating a liated by protease D-G, e.g. cancer, skin disorders, or neuropathic pain Nucleic acid encoding useful for identifying condition which is med

Claim 13; Fig 4B; 81pp; English

The invention relates to an isolated and purified nucleic acid that encodes a serine protease called D-G protein. The activity of the protein of the invention may be described as cytostatic, antiinflammatory, dermatological and anticoagulation. The serine protease of the invention is a member of the trypsin/chymotrypsin-like (S1) serine protease family, which play an important role in processes such as digestion and regulatory amplification cascades through the proteolytic activation of inactive zymogen precursors. Protease D-G modulating compounds are useful for treating a condition which is mediated by protease D-G, e.g. cancer, skin disorders, neuropathic path, inflammatory disorders, or coagulation diathesis/thrombosis. The polynucleotide encoding the protease is useful for identifying modulators of the functional protease. The D-G protein can be used for formulation of the functional protease. The D-G protein can be used for formulation of compositions for laundry detergents and skin care products. Protease Larget organisms. As the D-G protein is derived from a human, it is less likely to produce an allergic reaction in sensitive individuals when used in formulations for laundry detergents and skin care products. The current sequence represents the protease D-G cataytic domain in the zurrent sequence represents the protease D-G cataytic domain in the is a member of the try which play an importar regulatory amplificati for identifying, detecenceding the protease of the functional prot encodes a serine prote of the invention may } skin disorders, neuror diathesis/thrombosis. The invention relates target organisms. As likely to produce an in formulations for l D-G gene therapy may compositions for zymogen activation dermatological inactive of the of compo current

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                                                                 LLLLVVSNLLLCOGVVSDYKDDDDVDAAALAAPFDDDDKIVGGYALDV
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  100.0%; Score 1600; DB 23; Length 292; 100.0%; Pred. No. 7.5e-144; ive 0; Mismatches 0; Indels 0;
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WGYGCGGPSTPGVYTKVSAYLNWIYNVWKAELSRHHHHHHH

SVIBVVHWQQSQ

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Human; cancer; ulcer; HIV infection; human immunodeficiency virus;

mutiinflammatory; antirheumatic; antiarthritic; immunosuppressive;

mutibacterial; endocrine; cardiant; central nervous system; virucide;

muti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia;

muti-HIV; fungicide; antiallerary; antiulcer; osteopathic; eczema;

mutiaggregant; haemostatic; vulnerary; antiulcer; osteopathic; eczema;

dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic;

meuroprotective; antidepressant; nootropic; antiparkinsonian; inflammation;

meuroprotective; rheumatoid arthritis; septic shock; pancreatitis;

mutianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;

matianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;

matianaphylactic; seematopoietic disorder; platelet disorder; asthma;

thrombocytopaenia; osteoporosis; severe combined immunodeficiency;

mallergic rhinitis; diabetes; multiple sclerosis; depression;

mallergic rhinitis; diabetes; multiple sclerosis; depression;

mallergic rhinitis; diabetes; multiple sclerosis; depression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated human polynucleotides encoding polypeptides, useful for treatment and diagnosis of e.g. cancer, ulcers and HIV infection
                                                             Human protein sequence SEQ ID NO:1148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 20; Page 238; 1217pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Liu C, Drmanac RT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-DEC-1999; 99US-0471275.
21-JAN-2000; 2000US-0488725.
25-APR-2000; 2000US-0552317.
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                                                                                                                                                                                                                                                                                                              neurological disorder
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N-PSDB; AAH99574.
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AAM99166 to AAH99904 encode the human proteins given in AAM25255 to AAM25963. The proteins can have activities based on the tissues and cells they are expressed in, such as: antiinflammatory; antirheumatic; antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant; cantiavescular; antianaemic; antialergic; antimutagen; cardiovascular; antianaemic; antialergic; antiatherary; antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic; antiparkinsonian; and immunostimulant. The proteins and polynucleotides antiparkinsonian; and immunostimulant. The proteins and polynucleotides on production, The proteins and polynucleotides are useful for screening to production, The protein and for the treatment and diagnosis of disorders associated with the activity of a protein e.g. inflammation, rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction, neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal infections, autoimmunity, genetic diseases, haematopoietic disorders, anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers, anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers, catchinitis, asthma, diabetes, cancer, multiple sclerosis, depression, heurological disorders.

317 AA;

Gaps 0; Length 317; Indels 79.1%; Score 1266; DB 22; .larity 97.4%; Pred. No. 4.9e-112; Conservative 2; Mismatches 4; Query Match Best Local Similarity Matches 228; Conserv

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230
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                                                                                        263
                                           sphatases, proteases, transporters, transcription factors), useful for
PWQVSIQYDKQHVCGGSILDPHWVLTAAHCFRKHTDVFNWKVRAGSD
         sekwsdilloasvovidstrchaddavoesvrekomcaeipegevdic
                                                                     GKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPEGGVDTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   colon cancer, gastric cancer, sarcoma, lymphoma
                                                                                                                         <u> OWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL</u>
                                                                                                        QWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL
                                                                                                                                                                                                                                          profiling; expressed protein tag; EPT; kinase; protease; protease inhibitor; transporter; protein; receptor; transcription factor; cancer; mpatability complex; myeloma; colon cancer;
                                                                                                                                                                                                                                                                               sarcoma; melanoma; lymphoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 kinases, phosphatases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1582; 134pp; English.
                                                                                                                                                                                                                           (EPT) #1582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           receptors or
                                                                                                                                                                                                                                                                                                                                                                                                                                                              RG
                                                                                                                                                                      405
                                                                                                                                                                                                                                                                               arcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Urban
                                                                                                                                                                                                                                                                                                                                                                              79495P.
92544P.
10801P.
26370P.
36780P.
                                                                                                                                                                      tein;
                                                                                                                                                                                                                          Human expressed protein tag
                                                                                                                                                                                                                                                                                                                                                              2002WO-US09671
                                                                                                                                                                                                         entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ζ,
                                                                                                                                                                                                                                                                                                                                                                              2001US-275
2001US-292
2001US-310
2001US-326
2001US-336
                                                                                                                                                                                                                                                     phosphatase; protease;
cytoskeletal protein;
major histocompatabili
         :: | | | |
RVVGGEEASVDSW
                                                                                                                       OGDSGGPLMYOSD
KIVGGYALDVDSW
                                                  KLGSFPSLAVAKI
                                                                                                         OGDSGGPLMYQST
                                                                                                                                                                      standard; Pro
                                                                                                                                                                                                                                                                                cancer; adenoc
                                  KLGSFPSLAVAKJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polypeptides (e.g. cytoskeletal proteins, treating cancer, e.g. or leukemia
                                                                                     LWIIGWGFTKON
                                                                     LWIIGWGFTKON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 2; SEQ ID No
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tomlinson
                                                                                                                                                                                                        (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                            (ZYCO-) ZYCOS INC.
                                                                                                                                                                                                                                                                                                                           WO200278524-A2.
                                                                                                                                                                                                                                            Translational
                                                                                                                                                                                                                                                                                                                                                                              28-MAR-2001;
21-MAY-2001;
08-AUG-2001;
01-OCT-2001;
04-DEC-2001;
20-FEB-2002;
                                                                                                                                                                                                                                                                                                                                                              28-MAR-2002;
                                                                                                                                                                                                                                                                                                          sapiens
                                                                                                                                                                                                                                                                                                                                           10-OCT-2002
                                                                                                                                                                                                        29-JAN-2003
                                                                                                                                                                                                                                                                                         leukaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chicz RM,
                                                                                     204
                                                    144
                                                                                                                                                                                       ABU04916;
51
                84
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                                                                                                                                                                     ABU04916
                                                                                                                                                                                                                                                                               gastric
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The invention describes a purified polypeptide, which comprises a fragment of a kinase, phosphatase, protease, protease inhibitor, transporter, cytoskeletal protein, receptor or transcription factor. The polypeptide is useful as an immunogenic composition for eliciting in a mammal an immunogenic response directed against any of the purified polypeptide, or the antibody that binds to this polypeptide, is useful for treating cancer. The polypeptide is also useful for identifying compounds that binds to a naturally processed class I or class II MHC-binding polypeptide. The polypeptides and polynucleotides are particularly useful for treating or preventing

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myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma, lymphoma or leukaemia. These are also useful for screening agents for treating the above mentioned diseases. This sequence represents an expressed protein tag (BPT) isolated from human tissue for translational profiling.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polypeptides (e.g. kinases, phosphatases, proteases, transporters, cytoskeletal proteins, receptors or transcription factors), useful for treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma
                                                                                                                                                                                                                                                                                                                                                                               LWIIGWGFTKONGGKWSDILLQASVQVIDSTRCNADDAYQGEVTEKWMCAGIPEGGVDTC
                                                                                                                                                                                                                                        51 KIVGGYALDVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHCFRKHTDVFNWKVRAGSD
                                                                                                                                                                                                                                                         RVVGGEBRASVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHCFRKHTDVFNWKVRAGSD
                                                                                                                                                                                                                                                                                                 KLGSFPSLAVAKIIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFDEELTPATP
                                                                                                                                                                                                                                                                                                                   232 KLGSFPSLAVAKIIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFDEELTPATP
                                                                                                                                                                                                                                                                                                                                                          LWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPEGGVDTC
                                                                                      specification but
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                                                                                                                                                                                                                                                                                                                                                                                                                LMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                   QGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Translational profiling, expressed protein tag, EPT, kinase, phosphatase, protease, protease inhibitor, transporter, cytoskeletal protein, receptor, transcription factor, cancer, major histocompatability complex, myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma, lymphoma,
                                                                                                                                                                            5; DB 24; Length 405, 6.6e-112;
                                                                                                                                                                                                          Indels
                                                                                    Note: This sequence does not appear in the printed sobtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                          4
                                                                                                                                                                                                        2; Mismatches
                                                                                                                                                                             Score 1266;
Pred. No. 6.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human expressed protein tag (EPT) #1603.
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21-MAY-2001; 2001US-292544P.
08-AUG-2001; 2001US-310801P.
01-OCT-2001; 2001US-326370P.
04-DEC-2001; 2001US-336780P.
20-FEB-2002; 2002US-358985P.
                                                                                                                                                                            79.1%;
97.4%;
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                                                                                                                                                                                            Similarity
                                                                                                                                               405 AA;
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hes 228;
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leukaemia.
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                                                                                                                                                Sequence
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                                                          fragment of a kinase, phosphatase, profess, processe inhibitor, transporter, cytoskeletal protein, receptor or transcription factor. The polypeptide is useful as an immunogenic composition for eliciting in a mammal an immunogenic response directed against any of the purified polypeptide, or the antibody that binds to this polypeptide. The purified polypeptide, or the antibody that binds to this polypeptide, is useful for treating cancer. The polypeptide is also useful for identifying compounds that binds to a naturally processed class I or class II MHC-binding polypeptide. The polypeptides and polynucleotides are particularly useful for treating or preventing myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma, lymphoma or leukaemia. These are also useful for screening agents for treating the above mentioned diseases. This sequence represents an expressed protein tag (EPT) isolated from human tissue for translational
                                                                                                                                                                                                                                                                                                                                                                                                                         291
                                                                                                                                                                                                                            printed specification but was
                                                                                                                                                                                                                                                                                                                                                 51 KIVGGYALDVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHCFRKHTDVFNWKVRAGSD
                                                                                                                                                                                                                                                                                                                                                                                               IIIBFNPMYPKDNDIALMKLOFPLTFSGTVRPICLPFFDEELTPATP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL
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0
                                                                                                                                                                                                                                                                                                     Length 405;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            modulating protein; screening;
                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                            does not appear in the printed s
nic format directly from WIPO at
blished_pct_sequences.
                                                                                                                                                                                                                                                                                                  79.1%; Score 1266; DB 24;
97.4%; Pred. No. 6.6e-112;
ive 2; Mismatches 4;
                                                polypeptide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Transmembrane domain"
                          1603; 134pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        on/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               otein; 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Colorectal cancer; CGA7; CJA8; drug candidate; vaccine.
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                                                                                                                                                                                                                                                                                                                          Conservative
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Note: This sequence do
obtained in electronic
ftp.wipo.int/pub/publi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location 5..32 /note=
                                                                                                                                                                                                                                                                                                                                                                                               KLGSFPSLAVAKI
                                                                                                                                                                                                                                                                                                                                                                                                                                              LWIIGWGFTKONG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OGDSGGPLMYQSD
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06-SEP-2000; 2000US-06
                                                The invention describe
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RVVGGEEASVDSV
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Best Local Similarity
Matches 228; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard;
                                                                                                                                                                                                                                                                          405 AA;
                         SEQ ID
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or leukemia
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AG79358
X
C AAG79358;
X
C AAG79358;
X
X 21-AUG-200
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W Colorectal
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D 11-APR-200
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X 08-MAY-200
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C 08-MAY-200
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The sequences given in AAG79356-59 show the colorectal cancer proteins, CGA7 and CJA8 proteins are colorectal cancer modulating proteins and have been mapped to chromosomes 2 (CGA7) and I (CJA8). These sequences may be used in the method of the invention for screening drug candidates. The method comprises adding a drug candidate to a cell that expresses an expression profile gene. The new conding CGA7, CJA8 or fragments and determining the effect of the drug candidate on the expression of the expression profile gene. The new methods are used to screen bioactive agents for the ability to bind to or modulate the activity of CGA7 or CJA8 and evaluate the effect of a candidate colorectal cancer drug. An antibody to CGA7 or CJA8 can inhibit the activity of CGA7 or CJA8, respectively, and is used to screen for an agent that can interfere with the binding of CGA7 or CJA8 to the antibody can be used to treat colorectal cancer. The antibody or a fragment of it is used to localize a therapeutic group to antibody or a fragment of it is used to localize a therapeutic group to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a colorectal cancer tissue, where the therapeutic group is a cytotoxic agent or a radioisotope. Antisense molecules are used to inhibit colorectal cancer in a cell. Nucleic acid segments encoding CGA7 or CJA8 are used in a biochip. CGA7, CJA8 or a nucleic acid encoding it are used to elicit an immune response. CGA7 or CJA8 is used to determine the prognosis of an individual with colorectal cancer. Nucleic acid encoding CGA7 or CJA8 can be used in vaccines.
                                                                                                                                                                                                                                                                         Screening drug candidates for treating colorectal cancer, comprises determining the effect of the candidate on the expression profile gene of CGA7 or CJA8 -
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                                                                                                                     Wilson
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                                                                                                                                                                                                                                                                                                                                                                                              6; 40pp;
                                                                                                                                                                             WPI; 2002-453647/48.
N-PSDB; AAI72975.
MACK D.
GISH K C.
WILSON K E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
les 228; Conserv
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                                                                                                                       Gish KC,
                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig
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(MACK/)
(GISH/)
(WILS/)
                                                                                                                     Mack D,
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The invention relates to transmembrane serine proteases and their corresponding nucleotides and the protease domain of a type-II membrane-type serine protease (MTSP). MTSP is useful for identifying compounds that modulate or inhibits its proteolytic activity and for formulating a medicament for treating neoplastic disease. MTSP and its corresponding nucleotides are useful in preventing or treating tumours or cancers such as lung carcinoma, colon adenocarcinoma and ovarian carcinoma, in diagnostics and in hybridisation assays. MTSP is useful as a diagnostic marker for tumour development, growth and/or progression and as immunogens to generate antibodies that specifically bind to it. MTSP DNA is useful in a yeast two-hybrid system and in gene therapy. The present sequence is human transmembrane protease serine 4 (TMPRSS4) protein.
  neoplastic disease; tumour; cancer; cytostatic; adenocarcinoma; ovarian carcinoma; gene therapy; serine 4; TMPRSS4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel single chain polypeptide comprising protease domain of type-II membrane-type serine protease or its catalytically active portion useful for treating and preventing cancer and tumor
                                                                                                               .94
= "Conserved motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            English
                                                                                                  on/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 255-256; 256pp;
                                                                                                                                                                                                                                                         03-FEB-2000; 2000US-0179982.
18-FEB-2000; 2000US-0183542.
22-JUN-2000; 2000US-0213124.
26-JUL-2000; 2000US-0220970.
08-SEP-2000; 2000US-0657986.
22-SEP-2000; 2000US-0234840.
                                                                                                                                                                                                                                                                                                                                                                                                             Yeh J;
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190..19
/note=
MTSP; protease domain;
lung carcinoma; colon
transmembrane protease
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N-PSDB; AAD13169.
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                                                                Homo sapiens
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Region
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LWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPEGGVDTC
                                                                                                                                                                                                               KIGSFPSLAVAKIIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFDEELTPATP
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                                                                                         KIVGGYALDVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHCFRKHTDVFNWKVRAGSD
                                                                                                                            KLGSFPSLAVAKIIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFDEELTPATP
                                                                                                                                                                            LWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPEGGVDTC
                                                                                                                                            IIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFDEELTPATP
                                                                                                                                                                                                  LWIIGWGFTKONGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKNMCAGIPEGGVDTC
                                                     Gaps
                                                                                                                                                                                                                                   284
                                                                                                                                                                                                                                                           423
                                                                                                                                                                                                                                 DWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL
                                                                                                                                                                                                                                                 QGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL
                                                    0;
                          Length 423;
                                                  Indels
                        Score 1266; DB 22;
Pred. No. 7e-112;
2; Mismatches 4;
                                                 4,
                         79.1%;
97.4%;
cive 2
                      Query Match
Best Local Similarity 9'
Matches 228; Conservati
                                                                                                                                                                                                                            OGDSGGBTWXOSD
                                                                                                                                           KLGSFPSLAVAKI
423 AA;
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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention describes a method of diagnosing colorectal cancer comprising determining the expression of a gene encoding CJA8 or its fragment in a first colon tissue of an individual, and comparing the expression of the gene to the expression of the gene in normal tissue from the individual or in tissue from a second unaffected individual. A difference in the expression indicates that the first individual has colorectal cancer. The CJA8 genes and proteins are useful for diagnosing and prognosticating colorectal cancer. The methods are also useful for screening candidate bioactive agents that can modulate colorectal cancer, or for treating or inhibiting colorectal cancer in a patient e.g. by gene therapy. This is the amino acid sequence of the human colorectal cancer modulating protein CJA8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51 KIVGGYALDVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHCFRKHTDVFNWKVRAGSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KLGSFPSLAVAKIIIIBFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFDEELTPATP
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| RVVGGEEASVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHCFRKHTDVFNWKVRAGSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Diagnosing colorectal cancer comprises determining the expression of gene encoding CJA8 in a first colon tissue of a first individual, and comparing them to the expression of a gene encoding CJA8 in a second
                                                                                                                                                                 colorectal cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                modulating protein; BCMP; CJA8;
                                                                                                                               Human colorectal cancer modulating protein CJA8.
                                                                                                                                                                                                                                                                                  /note= "Encoded by ATC"
                                                                                                                                                                                                                                                  Location/Qualifiers
                               ABG72428 standard; Protein; 423 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 15; Fig 2; 31pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (EOSB-) EOS BIOTECHNOLOGY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wilson KE;
                                                                                                                                                                                                                                                                                                                                                                                                                   15-MAR-2000; 2000US-0525993.
28-JAN-2000; 2000US-0493444.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 97.4
                                                                                               (first
                                                                                                                                                                                  gene therapy; human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-066245/06.
N-PSDB; ABS57763.
                                                                                                                                                                 cancer
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                                                                                                                                                                Colorectal
                                                               ABG72428;
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                                                                                                                                                                                                                   Ношо
               ABG72428
RESULT
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QGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL

231

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The invention describes a purified polypeptide, which comprises a fragment of a kinase, phosphatase, protease, protease inhibitor, transporter, cytoskeletal protein, receptor or transcription factor. The polypeptide is useful as an immunogenic composition for eliciting in a mammal an immunogenic response directed against any of the purified polypeptide. The purified polypeptide, or the antibody that binds to this polypeptide, is useful for treating cancer. The polypeptide is also useful for identifying compounds that binds to a naturally processed class I or class II MHC-binding polypeptide. The polypeptides and polynucleotides are particularly useful for treating or preventing myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma, lymphoma or leukaemia. These are also useful for screening agents for treating the above mentioned diseases. This sequence represents an expressed protein tag (BPT) isolated from human tissue for translational
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 profiling.

Note: This sequence does not appear in the printed specification but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         kinases, phosphatases, proteases, transporters, receptors or transcription factors), useful for colon cancer, gastric cancer, sarcoma, lymphoma
              370 QGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL
                                                                                                                                                                                                                                        Translational profiling; expressed protein tag; EPT; kinase; phosphatase; protease inhibitor; transporter; cytoskeletal protein; receptor; transcription factor; cancer; major histocompatability complex; myeloma; colon cancer; gastric cancer; adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1584; 134pp; English
                                                                                                                                                                                                               n tag (EPT) #1584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AJ, Urban RG
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                                                                                                               Protein; 423
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92544P.
10801P.
26370P.
36780P.
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                                                                                                                                                                                 (first entry)
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21-MAY-2001; 2001US-2925
08-AUG-2001; 2001US-3108
01-OCT-2001; 2001US-3263
04-DEC-2001; 2001US-3367
20-FEB-2002; 2002US-3569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polypeptides (e.g. cytoskeletal proteins, treating cancer, e.g.
                                                                                                                                                                                                                   Human expressed protei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 2; SEQ ID No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chicz RM, Tomlinson
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                                                                                                              ABU04918 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                     WO200278524-A2
                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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Score 1266; DB 24; Length 423; Pred. No. 7e-112;

79.1%; 97.4%;

Query Match Best Local Similarity

Sequence

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polypeptides (e.g. kinases, phosphatases, proteases, transporters, cytoskeletal proteins, receptors or transcription factors), useful for treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or leukemia -
                                                                                                                                                                 RVVGGEEASVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHCFRKHTDVFNWKVRAGSD
                                                                                      KLGSFPSLAVAKIIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFDEELTPATP
                                                                                                      KLGSFPSLAVAKIIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFDEELTPATP
                            51 KIVGGYALDVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHCFRKHTDVFNWKVRAGSD
                                                                                                                                                  LWIIGWGFTKONGGKWSDILLOASVQVIDSTRCNADDAYQGEVTEKWMCAGIPEGGVDTC
 Gaps
                                                                                                                                                                                                             284
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                      Translational profiling; expressed protein tag; BPT; kinase; phosphatase; protease inhibitor; transporter; cytoskeletal protein; receptor; transcription factor; cancer; major histocompatability complex; myeloma; colon cancer; gastric cancer; adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
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                                                                                                                                                                                                                                                                                                                                                                                                               #1585,
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21-MAY-2001; 2001US-292544P.
08-AUG-2001; 2001US-310801P.
01-OCT-2001; 2001US-326370P.
04-DEC-2001; 2001US-336780P.
20-FBB-2002; 2002US-358985P.
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                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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and polynucleotides are particularly useful for treating or preventing myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma, lymphoma or leukaemia. These are also useful for screening agents for treating the above mentioned diseases. This sequence represents an expressed protein tag (EPT) isolated from human tissue for translational
                                                                                                                                                    specification but was
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51 KIVGGYALDVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHCFRKHTDVFNWKVRAGSD
                                                                                                                                                                                                                                                                                                                                                                                                                                            KLGSFPSLAVAKIIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFDEELTPATP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /SWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL
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                                                                                                                                                                                                                                                                                                            Length 423;
                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                  expressed protein tag (EPT) isolated from human tiss profiling.
Note: This sequence does not appear in the printed sobtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                            24;
                                                                                                                                                                                                                                                                                                          Score 1266; DB 24
Pred. No. 7e-112;
                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Translational profiling phosphatase, protease, cytoskeletal protein; rumajor histocompatability gastric cancer; adenocalleukaemia.
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                                                                        The invention describes a purified polypeptide, which comprises a fragment of a kinase, phosphatase, protease, protease inhibitor, transporter, cytoskeletal protein, receptor or transcription factor. The polypeptide is useful as an immunogenic composition for eliciting in a mammal an immunogenic response directed against any of the purified polypeptide, or the antibody that binds to this polypeptide, is useful for treating cancer. The polypeptide is also useful for identifying compounds that binds to a naturally processed class I or class II MHC-binding polypeptide. The polypeptides and polynucleotides are particularly useful for treating or preventing
                                                                                                                                                                                                                            myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma, lymphoma or leukaemia. These are also useful for screening agents for treating the above mentioned diseases. This sequence represents an expressed protein tag (BPT) isolated from human tissue for translational
                                                                                                                                                                                                                                                                                                 profiling.
Note: This sequence does not appear in the printed specification but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                51 KIVGGYALDVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHCFRKHTDVFNWKVRAGSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LWIIGWGFTKONGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPEGGVDTC
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gastric cancer, sarcoma, lymphoma
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                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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                                                                                                                                                                                                                                                                                                                                                                                                       Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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Pred. No. 7e-112;
                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Mismatches
                                                English
    colon cancer,
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                                                Example 2; SEQ ID No 1589; 134pp;
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98US-0098749.
98US-0098750.
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nilarity 97.4%;
Conservative 2
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es 228; Conserv
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       cancer,
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01-SEP-1998;
02-SEP-1998;
02-SEP-1998;
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                     or leukemia
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AAY99417
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New mammalian DNA sequences encoding transmembrane, receptor or secreted PRO polypeptides, useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wood
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.larity 97.4%; Pred. No. 7.1e-112;
Conservative 2; Mismatches 4;
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98US-0105002.
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98US-0108858.
98US-0108904.
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N-PSDB; AAA37099.
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21-0CT-1998;

22-0CT-1998;

25-0CT-1998;

26-0CT-1998;

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27-0CT-1998;

28-0CT-1998;

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                                          PWQVSIQYDKQHVCGGSILDPHWVLTAAHCFRKHTDVFNWKVRAGSD
                                       IIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFDEELTPATP
                                                                                                    LWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMCAGIPEGGVDTC
                                                                                       GKWSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPEGGVDTC
            QWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL 284
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2000US-189320P.
2000US-190828P.
2000US-191048P.
2000US-191048P.
2000US-191314P.
2000US-193053P.
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2000US-193053P.
2000US-194449P.
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2000US-19680P.
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2000WO-US05841.
2000US-187202P.
2000US-186968P.
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2000WO-US14941.
2000WO-US15264.
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KIVGGYALDVDSW
                                                                                      LWIIGWGFTKONG
                                                                                                                             OGDSGGPLMYQSD
                                                                                                                                              QGDSGGPLMYQSD
                                                                                                                                                                                                                                                        en
                                                                                                                                                                                                           AAU29188 standard; Pro
                                                                                                                                                                                                                                                                            Human PRO polypeptide
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                                                                                                                                                                                                                                                                                                                                                                             WO200168848-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2000;

02-MAR-2000;

06-MAR-2000;

14-MAR-2000;

15-MAR-2000;

21-MAR-2000;

21-MAR-2000;

21-MAR-2000;

21-MAR-2000;

21-MAR-2000;

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21-MAR-2000;

29-MAR-2000;

11-APR-2000;

                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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Sequences AAU29024-AAU2932B represent PRO polypeptides of the invention.
The PRO polypeptides and their associated nucleic acids can be used to detect the presence of a tumour in a mammal by comparing the level of expression of a PRO polypeptide in a test sample of cells from the animal acontrol sample of normal cells, whereby a higher level of expression in the test sample indicates the presence of a tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats and rabbits but are preferably human. The polypeptides can be used to stimulate tumour necrosis factor (TNF) alpha release from human blood, when contacted with it. A specific polypeptide can be used to stimulate the proliferation or differentiation of chondrocyte cells. The PRO proteins can be used to determine the presence of tumours and also susceptibility to tumour development, particularly adrenal, lung, colon, breast, prostate, rectal, cervical, or liver tumours, in mammalian subjects. The oligonucleotide probes specific for the PRO nucleic acids can be used for genetic analysis of individuals with genetic disorders.
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                                                                                                                                                                                                   Gurney AL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel nucleic acids encoding PRO polypeptides, used to diagnose the presence of tumours, such as prostate and breast tumours, in mammals to screen for modulators of the compounds -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPEGGVDTC
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                                                                                                                                                                                                   ₽J,
                                                                                                                                                                                                L, Goddard A, Godowski
Wood WI, Zhang Z;
                                                                                                                                                                                                                                                                                                                                                                                        Claim 11; Fig 330; 774pp; English.
                                                                                                                                                                                               J, Desnoyers L
, Watanabe CK,
05-JUN-2000; 2000US-209832P.
28-JUL-2000; 2000WO-US20710.
22-AUG-2000; 2000US-0644848.
24-AUG-2000; 2000WO-US23328.
08-NOV-2000; 2000WO-US30952.
01-DEC-2000; 2000WO-US32678.
                                                                                                                                                           (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                      WPI; 2001-602746/68.
N-PSDB; AAS46089.
                                                                                                                                                                                            KP, Chen J, Smith V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             432 AA;
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Best Local S
Matches 228
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Pan J,
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378

QGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL QGDSGGPLMYQSDQMHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL

319

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231 379 Protein;

AAB87581 standard;

mapping

Human; PRO protein;

Human PRO1570

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15-MAY-2001

AAB87581;

RESULT 13
AAB87581.
ID AAB8
XX
AC AAB8
XX
DT 15-P
XX
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XX
KW Huma

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The present sequence is a human PRO polypeptide (secreted and transmembrane). The PRO protein, and PRO agonists, PRO antagonists or anti-PRO antibodies are useful for preparation of a medicament useful in the treatment of a condition which is responsive to the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO protein may also be employed as molecular weight markers for protein electrophoresis. The PRO coding sequence has applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping.
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                                                                                                                                                                                                                                                                                                                                                                                                             c acids encoding PRO polypeptides, useful in including use as hybridization probes, and in
                                                                                                                                                                                                                                                                                                                                   Godowski PJ
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Wood WI;
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Watanabe
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AB66166
D AAB66166 standard; protein; 432 AA.
X
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                                                                                                               ; 99WO-US20111.
99WO-US21090.
99US-0169495.
99US-0170262.
; 2000WO-US04341.
; 2000WO-US04341.
; 2000WO-US04342.
; 2000WO-US06414.
; 2000WO-US05601.
; 2000WO-US05601.
; 2000WS-019397.
; 2000WS-0193397.
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97.4%;
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Grimaldi CJ, Gurney AL,
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Best Local Similarity
Matches 228; Conserv
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                                      WO200116318-A2
                                                                                                                 01-SEP-1999;
15-SEP-1999;
07-DEC-1999;
09-DEC-1999;
11-JAN-2000;
18-FEB-2000;
22-FEB-2000;
01-MAR-2000;
03-MAR-2000;
03-MAR-2000;
25-APR-2000;
05-UN-2000;
                                                                                         24-AUG-2000;
             Homo sapiens
                                                               08-MAR-2001
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318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KIVGGYALDVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHCFRKHTDVFNWKVRAGSD
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Hillan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Secreted and transmembrane proteins and nucleic acids designated useful as hybridization probes, in chromosome and gene mapping an
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Gurney AL,
A, Tumas D;
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owski PJ, Grimaldi CJ, Gu
4A, Smith V, Stewart TA,
PM, Wood WI;
                                                                                gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Fig 156; 787pp; English
                                                                                                                                                                                                                23-JUN-1999; 99US-0141037.
20-JUL-1999; 99US-0144758.
26-JUL-1999; 99US-0145698.
01-SEP-1999; 99US-0162506.
30-NOV-1999; 99WO-US28313.
02-DEC-1999; 99WO-US28313.
16-DEC-1999; 99WO-US28551.
16-DEC-1999; 99WO-US28551.
05-JAN-2000; 2000WO-US00219.
                                                                                                                                                                                                                                                                                                                                                                                                 Goddard A, Godowski Paoni NF, Roy MA, S CK, Williams PM, W
                                                    Protein of the invention #78
                                                                                                                                                                                           18-FEB-2000; 2000WO-US04342
                                                                                Secreted; transmembrane;
                                                                                                                                                                                                                                                                                                                                                                       (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-071395/08
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                                                                                                                                     WO200078961-A1.
                                                                                                                                                                                                                                                                                                                                                                                               Baker KP, Bot
Gao W, Goddar
Pan J, Paoni
Watanabe CK,
                                                                                                                                                               28-DEC-2000
                          02-APR-2001
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Human; secreted protein; transmembrane protein; antirheumatic; antiarthritic; osteopathic; sports-related joint problem; articular cartilage defect; osteoarthritis; rheumatoid arthritis.
                                                                                                                                                         Human secreted/transmembrane protein PRO1570
                                        ABG95906 standard; Protein; 432 AA
                                                                                                                                                                                                                                                                                                                                                                                             2001US-0006867
                                                                                                                    (first entry)
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2000WO-USS
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97US-064
98US-082
98US-089
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                                                                                                                                                                                                                                                                                                                                                                                                                                29-OCT-1997;
29-OCT-1997;
29-APR-1998;
15-MAY-1998;
10-JUN-1998;
10-JUN-1998;
11-JUN-1998;
11-JUN-1998;
12-JUN-1998;
14-MAY-1999;
16-JUN-1999;
16-JUN-1999;
16-JUN-1999;
16-SEP-1999;
15-SEP-1999;
18-FEB-2000;
22-MAY-2000;
23-AUG-2000;
23-AUG-2000;
23-AUG-2000;
23-AUG-2000;
20-DEC-2000;
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29-JUN-2001;
09-JUL-2001;
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                                                                                                                     10-DEC-2002
                                                                                                                                                                                                                                                                                                                                                        29-AUG-2002
                                                                              ABG95906;
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Godowski PJ; ď Goddard A Wood WI; ₩, ₩, Gerritsen Matanabe Filvaroff E Gurney Eaton DL, Fil Grimaldi JC,

WPI; 2002-731348/79 N-PSDB; ABS74433.

New isolated secreted and transmembrane PRO polypeptide userui for modulating biological activity of a cell, or for treating sports-related joint problems, osteoarthritis or rheumatoid arthritis

Claim 20; Fig 112; 399pp; English.

The invention relates to an isolated secreted and transmembrane PRO polypeptide having 80 % sequence identity to a sequence appearing as ABG95851-ABG95934 or their associated signal peptide, or a sequence of

c an extracellular domain of the proteins with their associated signal peptide or lacking its associated signal peptide. Also included are the nucleic acids encoding the proteins. Vectors, host cells the nucleic acids encoding the proteins. Vectors, host cells fusion proteins and antibodies which specifically bind to the proteins. The nucleic acids encoding the proteins. Vectors, host cells as a set useful for detecting a polypeptide designated as A, B, C or D in a sample suspected of containing an A, B, C or D polypeptide, D y contacting the sample with a polypeptide designated as B, F, G, H or I (or vice versa) and determining the formation of the formation of the presence of an A, B, C or D polypeptide in the sample, where A is a PRO1096 polypeptide, B is a PRO20010 polypeptide, B is a PRO20010 polypeptide, B is a PRO20010 polypeptide, B is a PRO20010 polypeptide, B is a PRO20010 polypeptide and I is a PRO30010 polypeptide and I is a PRO30010 polypeptide. The B, C, G, H or I polypeptide is labeled with B, C or D polypeptide. The B, C, B, C, H or I polypeptide is labeled with C adetectable label or is attached to a solid support. The proteins are useful for linking a bioactive molecule to a codi, ry He bioactive molecule is a toxin, a radiolabel or an antibody. The bioactive of against them are useful for modulating a biological activity of a cell expressing a polypeptide designated as A, B, C or D or B, F, G, H, or I. The cell is killed. The proceins are useful for identifying a polypeptide designated as A, B, C or D or B, F, G, H, or I. The cell is killed. The proceins are useful for identifying a causes death. of the proceins are useful as A, B, C or D or B, F, G, H, or I. The cell is killed. The proceins are useful of the proteins, as molecular weight markers for proteins are useful a with process, and as the treatment of a condition which is responsive to the proteins, as a therapeutic agents for treating sports-ralated joint problems.

The cell x wight markers for protein electrophores is purposes, and secreted or transmembrane protein of the invention 

432 AA; Sequence

o; 110 258 170 230 378 199 RVVGGEBASVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHCFRKHTDVFNWKVRAGSD 259 KLGSFPSLAVAKIIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFDEELTPATP 51 KIVGGYALDVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHCFRKHTDVFNWKVRAGSD LWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPEGGVDTC LWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPEGGVDTC KLGSFPSLAVAKIIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFDEELTPATP QGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL 432 QGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL 284 ٥; 79.1%; Score 1266; DB 23; Length 432; larity 97.4%; Pred. No. 7.1e-112; Conservative 2; Mismatches 4; Indels 0 Similarity Query Match Best Local Simi Matches 228; 111 171 319 231 379

g  $\delta$ g ò ga  $\delta$  completed: November 23, 2003, 07:49:06 : 43.9766 secs time

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; 2003, 07:47:10 ; Search time 14.8611 Seconds (without alignments) 831.351 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                     328717
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1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                otal number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ost-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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erfect score:
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	Description	Sequence 2,	Sequence 6.	Sequence 9,	Segmence 9.	Sequence 11	Sequence 8,	ш	۲	ເດ	equence 1	equence 5		equence 8	equence 8	9	equence 1	Ŋ	Sequence 2,	Sequence 2,	Sequence 2,	Sequence 4,	Seguence 3,	Sequence 3,	Segmence 67	equence 1	Sequence 1,	/
SUMMARIES	ID	1 1	US-09-008-271A-6	•	-986-60-	9-986-60-	-09-386-62	US-09-386-642-14	09-386-64	US-09-386-642-53	42-1	542	08~508-448C	338-	-09-370-838	0-838	US-08-508-448C-19	US-09-518-046-2	0	59-60-	39-820-	09-820-00	US-09-027-337-3	4-60	US-08-944-483-67	7-15	US-09-478-957-1	
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	Query Match Length	423	435	316	315	328	327	289	288	306	319	284	418	418	418	418	232	454	492	492	376	417	256	256	255	283	283	
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Sequence 3, Appli	Sequence 26, Appl			Sequence 68, Appl	4, A	9	7	Sequence 2, Appli	m	4	7	7	13	7.	, <del>,</del>	, ,i	Sequence 1, Appli
US-08-681-151-3	US-09-023-942A-26	US-08-944-483-63	US-08-978-404B-44	US-08-944-483-68	US-09-734-675-4	US-09-023-942A-6	US-09-387-375-7	US-08-956-267A-2	US-09-008-271A-3	US-09-023-942A-4	US-09-027-337-2	US-09-644-600-2	US-08-991-761A-13	US-09-386-653A-7	US-08-248-629A-1	US-08-451-932-1	US-08-452-260-1
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638	285	248	246	250	407	314	284	247	314	312	855	855	790	290	812	812	812
30.6	30.1	29.8	29.0	29.0	28.8	28.5	28.4	28.3	28.2	28.2	27.8	27.8	27.7	27.7	27.6	27.6	27.6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            250 KLGSFPSLAVAKIIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFDEELTPATP
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         US-99-58-002-2.

Sequence 2, Application US/09656002

Fatent No. 645568

GENERAL INFORMATION:

APPLICANT: Mack, David

APPLICANT: Wilson, Keith

TITLE OF INVENTION: OF SCREENING FOR COLORECTAL CANCER, COMP

TITLE OF INVENTION: OF SCREENING FOR COLORECTAL CANCER, COMP

TITLE OF INVENTION: OF SCREENING FOR COLORECTAL CANCER MODULATORS

FILE REFERENCE: A-69108/DJB/JJD/AMS

CURRENT APPLICATION NUMBER: US 09/656,002

CURRENT FILING DATE: 2000-03-15

FRIOR FILING DATE: 2000-01-28

FRIOR PELING DATE: 2000-01-28

FRIOR FILING DATE: 2000-03-15

NUMBER OF SEQ ID NOS: 3

SOFTWARE: Patentin version 3.0

LENGTH: 423

LENGTH: 423

TYPE: PRT

ORGANISM: Home sapiens

US-09-656-002-2
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Pred. No. 5.5e-128;
2; Mismatches 4;
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Best Local Similarity 97.4%;
Matches 228; Conservative ;
US-09-656-002-2
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RESULT 2 US-09-008-271A-6

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|S-09-387-375-9
|Sequence 9, Application US/09387375
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61 GEWPWQASIQHPGAHVCGGSLIAPQWVLTAAHCFPRRALPAEYRVRLGALRLGSTSPRTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SLAVAKIIIIEFNPMYPKD---NDIALMKLQFPLTFSGTVRFICLPFFDEELTPATPLWI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    225 GGVDTCQGDSGGPL-MYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Description of Artificial Sequence: Fusion Protein OTHER INFORMATION: of Protease T in a zymogen activation construct US-09-386-653A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 DSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHCFRKHTDVFNWKVRAGSDKLGSFP--
                                                                                                                                                                                                                                                                                                                                                                             ) OTHER INFORMATION: Description of Artificial Sequence: Amino acid; OTHER INFORMATION: Sequence of EOS zymogen fusion gene US-09-387-375-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9, Application US/09386653A

Sequence 9, Application US/09386653A

Patent No. 6458564

GENERAL INFORMATION:

APPLICANT: Andrade-Gordon, Patricia

APPLICANT: Darrow, Andrew

APPLICANT: Oi, Jian-shen

TITLE OF INVENTION: DNA encoding the novel human serine

TITLE OF INVENTION: protease T

TITLE OF INVENTION: protease T

FILE REFERENCE: ORT-1032

CURRENT APPLICATION NUMBER: US/09/386,653A

CURRENT FILING DATE: 1999-08-31

NUMBER OF SEQ ID NOS: 11

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 9

LENGTH: 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 Score 765; DB 4; Length 31 Similarity 51.1%; Pred. No. 3.4e-74; 54; Conservative 38; Mismatches 85; Indels
                                                                                                                                Human Serine
                   Patent No. 6485957

GENERAL INFORMATION:

APPLICANT: Darrow, Andrew
APPLICANT: Andrade-Gordon, Patricia
APPLICANT: Qi, Jenson
TITLE OF INVENTION: DNA Encoding the Human S
TITLE OF INVENTION: Protease EOS
FILE REFERENCE: ORT-1031
CURRENT APPLICATION NUMBER: US/09/387,375
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
LENGTH: 316
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
FEATURE:
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ORGANISM: Artificial Sequence
FRATURE:
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Best Local Simi:
Matches 164;
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                                                                                                                                                                                                                                                                                                     ADDRESSES: INCYCE FRAIMACEUTICALS, INC.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/008,271A
FILING DATE: 16-Jan-1998
PRIOR APPLICATION NUMBER: <UNKnown>
                                                                                                                                                                             Shah, Purvi
TITLE OF INVENTION: HUMAN PROTEASE MOLECULES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1266; DB 3;
Pred. No. 5.7e-128;
2; Mismatches 4;
                                                                                                                                                                                                                                                                            Incyte Pharmaceuticals, Inc. 74 Porter Dr. Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Mohan-Peterson, Sheela
REGISTRATION NUMBER: 41,201
REFERENCE/DOCKET NUMBER: PF-0458 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18
ION: SEQ ID NO:
ERISTICS:
amino acids
                                                                                               Hillman, Jenniter
Yue, Henry
Guegler, Karl J.
Corley, Neil C.
Tang, Tom Y.
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97.4%; Pred
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NO: 6:
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SEQUENCE DESCRIPTION
'S-09-008-271A-6
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INFORMATION FOR SEQ ID
SEQUENCE CHARACTER
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Best Local Similarity
Matches 228; Conser
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RESULT 7
US-09-386-642-14
; Sequence 14, Application US/09386642
; Patent No. 6420157
; GENERAL INFORMATION:
; APPLICANT: Darrow, Andrew
; APPLICANT: Qi, Jenson
; APPLICANT: Andrade-Gordon, Patricia
; TITLE OF INVENTION: Zymogen Activation System
; FILE REFERENCE: ORT-1028
; CURRENT APPLICATION NUMBER: US/09/386,642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --AELSRHHHHHH 292
                                                 -----NVWKAEL---SRHHHHHH 292
                                                                             301 PQTQESQPDSNLCGSHLAFSSRHHHHHH 328
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Patent No. 6426199
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Best Local Similarity
Matches 164; Conserva
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                                                                                                                                                                                                      FEEGKKDACKGDSGGPLVCLVGQSWLQAGVISWGEGCARQNRPGVYIRVTAHHNWIHRII 293
                                                                                                                          DSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHCFRKHTDVFNWKVRAGSDKL-GSFPSLA 119
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                                                                                                                                                                                     ---PKDNDIALMKLQFPLTFSGTVRPICLPFFDEELTPATPL--WII
                                                                                                                                                                                                                                                                     IPEGGVDTCQGDSGGPLMYQSDQ-WHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNV-
                                                             MDSKGSSQKSRLLLLLVVSNLLLCQGVVSDYKDDDDVDAAALAAPFDDDDKIVGGYALDV
                                                                                       1 MDSKGSSQKSRILILILVVSNILLCQGVVSDYKDDDDVDAAALAAPFDDDDKIVGGYALBE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GFTKQNGGKMS-DILLQASVQVIDSTRCNA---DDAYQGE---VTEKMMCAGIPEGGVDT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Description of Artificial Sequence: Fusion gene OTHER INFORMATION: with homo sapien serine protease catalytic domain S-09-386-642-11
                               37;
    Length 315;
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                               Indels
    DB 4;
Query Match
Best Local Similarity 48.4%; Pred. No. 4.6e-73;
Matches 156; Conservative 46; Mismatches 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Darrow, Andrew
APPLICANT: Qi, Jenson
APPLICANT: Qi, Jenson
TITLE OF INVENTION: Zymogen Activation System
FILE REFERENCE: ORT-1028
CURRENT APPLICATION NUMBER: US/09/386,642
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 60
                                                                                                                                                                                                                                                                                                                                                                            ----WKAELSRHHHHHH 292
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LENGTH: 328
TYPE: PRT
ORGANISM: Artificial Sequence
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S-09-386-642-11
Sequence 11, Application
Patent No. 6420157
GENERAL INFORMATION:
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Best Local Similarity
Matches 163; Conser
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Darrow, Andrew L.

APPLICANT: Qi, Jenson

APPLICANT: Qi, Jenson

TITLE OF INVENTION: Idenification and Characterization of the complementary

TITLE OF INVENTION: DNA encoding the novel human serine protease C-E

FILE REFERENCE: ORT-1030

CURRENT APPLICATION NUMBER: US/09/386,629

CURRENT FILING DATE: 1999-08-31

NUMBER OF SEQ ID NOS: 11

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 8

LENGTH: 327

TYPE: PRT

ORGANISM: Artificial Sequence
                                 281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 SEWPWIVSIQKNGTHHCAGSLLTSRWVITAAHCFKDNLNKPYLFSVLLGAWQLGN-PGSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   174 IGWGFTKONGGKM--SDILLQASVQVIDSTRCNA---DDAYQGEVTEKMMCAGIPEGGVD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 VAKIII--IEFNPMYP-KDN---DIALMKLQFPLTFSGTVRPICLPFFDEELTPATPLWI
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    COGDSGGPLMYQSD-QWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIY-
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49.8%; Pred. No. 1.6e-71;
tive 39; Mismatches 87;
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RESULT 10
US-09-386-642-12
; Sequence 12, Application US/09386642
; Patent No. 6420157
; GENERAL INFORMATION:
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Best Local Similarity 42.9
Matches 126; Conservative
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                                                                                                                                                                                                                                                                                               1 MDSKGSSQKSRLLLLLVVSNLLLCQGVVSDYKDDDDVDAAALAAPFDDDDKIVGGY-ALD
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                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence: Fusion gene OTHER INFORMATION: with homo sapien serine protease catalytic domain S-09-386-642-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence: Fusion OTHER INFORMATION: with homo sapien serine protease catalytic S-09-386-642-13
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                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                       42.0%; Score 672.5; DB 4;
48.5%; Pred. No. 2.8e-64;
ive 39; Mismatches 89;
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CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 14
LENGTH: 289
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                                                                                          TYPE: PRT ORGANISM: Artificial Se
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Sequence 13, Application
Patent No. 6420157
GENERAL INFORMATION:
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ORGANISM: Artificial
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Best Local Similarity
Matches 148; Conserv
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Best Local Similarity
Matches 146; Conser
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LENGTH: 288
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136
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                                                                                                             EQEIPVVQSIP---HPCYNSSDVEDHNHDLMLLQLRDQASLGSKVKPISLA--DHCTQPG
                                                                                                                                                                              TPLWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKWMCAGIPEGGVD
                                                                                                                                                                                                           : | | | : | : | : | | | : | : | 170 QKCTVSGWGTVTSPRENFPDTLNCAEVKIFPQKKC--EDAYPGQITDGWVCAGSSK-GAD
                                                                                                                                                                                                                                                                                TCQGDSGGPLMYQSDQWHVVGIVSWGYG-CGGPSTPGVYTKVSAYLNWIYNVWKAELSRH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 53, Application US/09386642
; Retent No. 6420157
; GENERAL INFORMATION:
; APPLICANT: Darrow, Andrew
; APPLICANT: Qi, Jenson
; TITLE OF INVENTION: Zymogen Activation System
; FILE REFERENCE: ORT-1028
; CURRENT APPLICATION NUMBER: US/09/386,642
; CURRENT FILING DATE: 1999-08-31
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 53
; LENGTH: 306
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human protease F in CFEK2 zymogen vector
US-09-386-642-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37;
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42.9%; Pred. No. 1.3e-56;
iive 46; Mismatches 85;
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l Similarity 41.8
97; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
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STATE:
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Matches 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ICLPFFDEELTPATPLWIIGWGFTKQNGGKMS-DILLQASVQVIDSTR 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CKILYNIDAKPEEPHFVQEDMVCAGYVEGGKDACQGDSGGPLSCPVEGLWYLTGIVSWGD 258
                                                                                                                                                                                                                                                                                                                                                                VSDYKDDDDVDAALAAPFDDDDKIVGGYALDVDSWPWQVSIQYDKQHVCGGSILDPHWV 87
                                                                                                                                                                                                                                                                                                                                                                                  -----SRHHHHH
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                                                                                                                                                                                                                                                                                                                                   38; Gaps
                                                                                                                                                                                                                                 OTHER INFORMATION: Description of Artificial Sequence: Fusion gene OTHER INFORMATION: with homo sapien serine protease catalytic domain 8-09-386-642-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Description of Artificial Sequence: Human MH2 OTHER INFORMATION: protease in PFEK zymogen vector
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                                                                                                                                                                                                                                                                                               37.1%; Score 593; DB 4; Length 319; 44.2%; Pred. No. 1.2e-55; ive 35; Mismatches 95; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 54, Application US/09386642
Patent No. 6420157
GENERAL INFORMATION:
APPLICANT: Darrow, Andrew
APPLICANT: Darrow, Andrew
APPLICANT: Qi, Jenson
APPLICANT: Andrade-Gordon, Patricia
TITLE OF INVENTION: Zymogen Activation System
FILE REFERENCE: ORT-1028
CURRENT APPLICATION NUMBER: US/09/386,642
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.0
APPLICANT: Darrow, Andrew APPLICANT: Qi, Jenson APPLICANT: Qi, Jenson APPLICANT: Andrade-Gordon, Patricia TITLE OF INVENTION: Zymogen Activation System FILE REFERENCE: ORT-1028 CURRENT APPLICATION NUMBER: US/09/386,642 CURRENT FILING DATE: 1999-08-31 NUMBER OF SEQ ID NOS: 60 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KVSAYLNWIY---
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|139 SRPITFSRYIRD
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                                                                                                                                                                LENGTH: 319
TYPE: PRT
ORGANISM: Artificial
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Best Local Similarity
Matches 133; Conser
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Best Local Similarity
Matches 133, Conser
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LENGTH: 284
TYPE: PRT
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S-09-386-642-54
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Sequence 25, Application US/08508448C

Sequence 25, Application US/08508448C

Patent No. 5804410

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Kazuyoshi YAMAOKA et al.

TITLE OF INVENTION: NUCLEIC ACID SEQUENCE ENCODING

TITLE OF INVENTION: TRYPSIN-LIKE ENZYME AND PROCESS FOR PRODUCING THE BNZYME

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: Wenderoth, Lind & Ponack

STREET: 805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                  61 PHSQPWQAALVMENELFCSGVLVHPQWVLSAAHCFQN----SYTIGLGLHSLEADQEPG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GWGFTKQNGGKWSDIJLQASVQVIDSTRCNA--DDAYQGEVTEKMMCAGIPEGGVDTCOG 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    228 DSGGPLICNG---YLQGLVSFGKAPCGQVGVPGVYTNLCKFTEWIEKTVQAS-SRHHHHH 283
                                                                                                                                                                                                                                                  60 VDSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHCFRKHTDVFNWKVRAGSDKL--GSFPS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118 LAVAKIIIIEFNPMYPKD---NDIALMKLOFPLTFSGTVRPICLPFFDEELTPATPLWII 174
                                                                                          1 MDSKGSSOKSKLILLLVVSNLLLCOGVVSDYKDDDDVDAAALAAPFDDDDKIVGGYNCLE 60
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1 MDSKGSSQKSRLLLLLVVSNLLLCQGVVSDYKDDDDVDAAALAAPFDDDDKIVGGY-ALD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        233 DSGGPLMYQSDQMHVVGIVSWGYG-CGGPSTPGVYTKVSAYLNWIYNVWKAELSRHHHHH
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41.8%; Pred. No. 2.5e-48;
tive 49; Mismatches 79;
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CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/508,448C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Warren M. Cheek, Jr. REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
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N: 435
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COMPUTER READABLE FORM:
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APPLICATION NUMBER:
FILING DATE:
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                                                                                                                                                                                        360
                                                                         166
                                                                                              244 IST--TFPKLRMRVRNILIHNNYKSATHENDIALVRLENSVTFTKDIHSVCLPAATQNIP 301
                                                                                                                                                                      | : :: | | : : | | :: | | :: | : | | :: | 302 PGSTAYVTGWGAQEYAGHTVPE-LRQGQVRIISNDVCNAPHSYNGAILSGMLCAGVPQGG
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                 49 DDKIVGGYALDVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHCFRKHTDVFNWKVRAG
                                                                                                                                                  PATPLWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPEGG
                                                                         VAKIIIIBFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFDEBLT
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                                                                                                                                                                                                                                                 Length 418;
                                                                                                                                                                                                                                                                                                                                                      Sequence 82, Application US/09370838
Sequence 82, Application US/09370838
Patent No. 6444425
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Mohamath, Roadoh
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF
TITLE OF INVENTION: LUNG CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.475C1
CURRENT FILING DATE: 1999-08-09
EARLIER PILING DATE: 1999-08-09
EARLIER PILING DATE: 1999-04-02
NUMBER OF SEQ ID NOS: 289
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 82
LENGTH: 418
TYPE: PRT
ORGANISM: Homo sapien
S-09-370-838-82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      THERAPY AND DIAGNOSIS
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11.8%; Pred. No. 2.5e-48;
ive 49; Mismatches 79;
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POUNDS FOR
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Patent No. 6444425
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Mohamath, Roadoh
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOUNDS
                                                                          SDKLGSFPSL--A
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Best Local.Similarity
Matches 97; Conser
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S-09-370-838-83
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S-09-370-838-82
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; Fatent No. 6444425
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Lodes, Michael J.
APPLICANT: Mohamath, Roadch
; APPLICANT: Mohamath, Roadch
; APPLICANT: Mohamath, Roadch
; TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF
; TITLE OF INVENTION: LOMPOUNDS FOR THEIR USE
; TITLE OF INVENTION: LOMPOUNDS FOR THEIR USE
; TITLE OF INVENTION: LOMPOUNDS FOR THEIR USE
; TITLE REFERENCE: 210121.475C1
; CURRENT APPLICATION NUMBER: US/09/370,838
; CURRENT FILING DATE: 1999-08-09
; BARLIER APPLICATION NUMBER: US 09/285,323
; BARLIER FILING DATE: 1999-04-02
; NUMBER OF SEQ ID NOS: 289
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 62
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-370-838-62
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Best Local Similarity 41.4%; Pred. No. 4.1e-48;
Matches 96; Conservative 50; Mismatches 79;
          FOR
; TITLE OF INVENTION: LUNG CANCER AND METHODS |
; FILE REFERENCE: 210121.475C1
; CURRENT APPLICATION NUMBER: US/09/370,838
; CURRENT FILING DATE: 1999-08-09
; EARLIER APPLICATION NUMBER: US 09/285,323
; EARLIER FILING DATE: 1999-04-02
; NUMBER OF SEQ ID NOS: 289
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 83
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-370-838-83
                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
          METHODS
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Best Local Similarity 41.8
Matches 97; Conservative
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US-09-370-838-62
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302 PGSTAYVTGWGAQEYAGHTVPE-LRQGQVRIISNDVCNAPHSYNGAILSGMLCAGVPQGG 360

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- - 23, 2003, 07:53:47 earch completed: November ob time: 15.8611 secs

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2003, 07:49:15; Search time 18.4759 Seconds (without alignments)
2885.234 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 6, Appli Sequence 72, Appl	23.	2.	7	27	275.	112.	275.	330	275	, 0 %	, 000	, 0	
	SUMMARIES	US-09-851-588-6 US-09-776-191-72	US-10-264-820-23	US-10-254-289-2	US-09-888-257A-7	US-09-946-374-275	US-10-015-387A-275	US-10-063-735-112	US-10-006-130A-275	US-10-199-672-330	US-10-006-172A-275	US-10-187-749-330	US-10-194-457-330	US-10-184-642-330	US-10-196-747-330
	DB	9	15	15	11	11	12	12	12	12	77	7	12	12	12
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	% Query Match	79.1	79.1	79.1	79.1	79.1	79.1	79.1	79.1	79.1	79.1	79.1	79.1	79.1	79.1
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US-09-851-588-6

i Sequence 6, Application US/09851588

j Patent No. US20020042067A1

j GENERAL INFORMATION:

APPLICANT: Mack, David

APPLICANT: Wilson, Keith E.

ITILE OF INVENTION: NOVEL METHODS OF DIAGNOSING COLORECTAL CANCER, COMI

TITLE OF INVENTION: OF SCREENING FOR COLORECTAL CANCER MODULATORS

FILE REFERENCE: A-68829-1/DJE/JJD/AMS

CURRENT FILING DATE: 2001-09-24

PRIOR APPLICATION NUMBER: US 09/642,252

PRIOR APPLICATION NUMBER: US 09/656,002

PRIOR APPLICATION NUMBER: US 09/656,002

PRIOR FILING DATE: 2000-09-06

NUMBER OF SEQ ID NOS: 9

SOFTWARE: Patentin version 3.1

SEQ ID NO 66
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Pred. No. 5.8e-117;
2; Mismatches 4;
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228; Conservative
                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 406
TYPE: PRT
ORGANISM: Homo sapiens
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TYPE: PRT
ORGANISM: Homo sapiens
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Sequence 23, Application US/10264820
Publication No. US20030108926A1
GENERAL INFORMATION:
APPLICANT: Eos Biotechnology, Inc.
TITLE OF INVENTION: Compositions, and Methods of Screening for Colorectal
TITLE OF INVENTION: Cancer Modulators
FILE REFERENCE: 018501-006141US
FULE REFERENCE: 018501-006141US
                                                                                                                                                                                                                               ESULT 2
S-09-776-191-72
Sequence 72, Application US/09776191
Publication No. US20030119168A1
GENERAL INFORMATION:
APPLICANT: Eddwin L. Madison
APPLICANT: Eddwin L. Madison
APPLICANT: Eddwin L. Madison
APPLICANT: Juun-Chern Yeh
APPLICANT: Orivas International, Inc.
TITLE OF INVENTION: TRANSWEMBRANS SERINE PROTEASES, THE ENCODED PROTEINS AND TITLE OF INVENTION: METHODS BASED THEREON
TITLE OF INVENTION: METHODS BASED THEREON
TITLE OF INVENTION: METHODS BASED THEREON
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FILE REFERENCE: 2445-160,
CURRENT FILING DATE: 2001-02-02
PRIOR FILING DATE: 2000-02-03
PRIOR FILING DATE: 2000-02-03
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Best Local Similarity
Matches 228; Conser
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S-09-776-191-
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Sequence 2, Application US/10254289

Publication No. US20030118509A1

GENERAL INFORMATION:

APPLICANT: Gish, Kurt

APPLICANT: Wilson, Keith

TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSING COLORECTAL CANCER, COMPOSITIONS, AND N

TITLE OF INVENTION: OF SCREENING FOR COLORECTAL CANCER MODULATORS

TITLE OF INVENTION: OF SCREENING FOR COLORECTAL CANCER MODULATORS

FILE REFERENCE: A-69108/DJB/JJD/AMS

CURRENT APPLICATION NUMBER: US/10/254,289

CURRENT APPLICATION NUMBER: US/09/656,002

PRIOR FILING DATE: 2000-09-06

PRIOR FILING DATE: 2000-03-15

PRIOR FILING DATE: 2000-01-28

PRIOR FILING DATE: 2000-01-28

PRIOR FILING DATE: 2000-03-15

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Pred. No. 6.1e-117;
2; Mismatches 4;
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: US 09/268,866
PRIOR FILING DATE: 1999-03-15
PRIOR FILING DATE: 1999-03-15
PRIOR APPLICATION NUMBER: US 09/436,945
PRIOR FILING DATE: 1999-11-09
PRIOR FILING DATE: 1999-11-09
PRIOR FILING DATE: 1999-11-09
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: US 09/453,850
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: US 09/453,444
PRIOR FILING DATE: 2000-01-28
PRIOR FILING DATE: 2000-01-28
PRIOR FILING DATE: 2000-03-15
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PATENTIN VEY: 2.1
SEQ ID NO 23
LENGTH: 423
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Best Local Similarity 97.4%;
Matches 228; Conservative 2
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US-10-264-820-23
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                                                            Length 423;
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                                                       Score 1266; DB 15;
Pred. No. 6.1e-117;
2; Mismatches 4;
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APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Golakis, Paul J.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Mith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Warner Semin
TITLE OF INVENTION: COMPOSITIONS AND METHODS J
TITLE OF INVENTION: TREATMENT OF TUMOR
FILE REFERENCE: PSOO2R1
CURRENT APPLICATION NUMBER: US 60/063,540
PRIOR FILING DATE: 1998-00-10
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: US 60/089,653
PRIOR FILING DATE: 1998-00-00
PRIOR FILING DATE: 1998-00-00
PRIOR FILING DATE: 1998-00-01
PRIOR FILING DATE: 1999-06-01
PRIOR FILING DATE: 1999-06-01
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PRIOR APPLICATION NUMBER: PCT/US00/23328
PRIOR PRIOR DATE: 2000-03-08
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PRIOR APPLICATION NUMBER: PCT/US00/23328
PRIOR PRIOR DATE: 2000-03-08
PRIOR APPLICATION NUMBER: PCT/US00/23328
PRIOR PRIOR DATE: 2000-03-03
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PRIOR FILING DATE: 2001-03-01
NUMBER OF SEQ ID NOS: 10
SEQ ID NO 7
LENGTH: 432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7, Application US/09888257A Publication No. US20030060612A1 GENERAL INFORMATION:
                                                       Query Match
Best Local Similarity 97.4%;
Matches 228; Conservative
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S-09-888-257A-7
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APPLICANT: Pan, undes
APPLICANT: Pan, undes
APPLICANT: Roy, Margaret Ann
APPLICANT: Roy, Margaret Ann
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides
APPLICANT: Wood, William I.
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2830PLG1
CURRENT FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098723
PRIOR APPLICATION NUMBER: 60/098723
PRIOR APPLICATION NUMBER: 60/098720
PRIOR FILING DATE: 1998-09-01
PRIOR FILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/098821
PRIOR APPLICATION NUMBER: 60/098821
PRIOR APPLICATION NUMBER: 60/098821
PRIOR APPLICATION NUMBER: 60/098821
PRIOR APPLICATION NUMBER: 60/098821
PRIOR APPLICATION NUMBER: 60/098821
PRIOR FILING DATE: 1998-09-02
PRIOR FILING DATE: 1998-09-09
PRIOR FILING DATE: 1998-09-09
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                                                                                                                                                                Gaps
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                                                                                                Length 432;
                                                                                                                                                             Indels
                                                                                           Query Match

79.1%; Score 1266; DB 11;

Best Local Similarity 97.4%; Pred. No. 6.3e-117;

Matches 228; Conservative 2; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Baker, Kevin P.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Baton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Paul J.
APPLICANT: Grimaldi, Christopher J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 275, Application US/09946374 Publication No. US20030073129A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gurney, Austin L. Hillan, Kenneth J
; ORGANISM: Homo Sapien
US-09-888-257A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pan, James
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PRIOR APPLICATION NUMBER: 60/10147
PRIOR PLILING DATE: 1998-09-33
PRIOR PLILING DATE: 1998-09-24
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PRIOR PLILING DATE: 1998-10-01
PRIOR PLILING DATE: 1998-10-07
PRIOR APPLICATION NUMBER: 60/10339
PRIOR PLILING DATE: 1998-10-07
PRIOR PLILING DATE: 1998-10-07
PRIOR PLILING DATE: 1998-10-07
PRIOR PRILING DATE: 199

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Godowski, Paul J.
Grimaldi, Christopher
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US-10-063-735-112
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APPLICANT: Gao, Wei-Qiang
APPLICANT: Gao, Wei-Qiang
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Pani, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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                                                                                                                                                         Length 432;
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                                                                                                                                                    79.1%; Score 1266; DB 11;
larity 97.4%; Pred. No. 6.3e-117;
Conservative 2; Mismatches 4;
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CURRENT FILING DATE: 2001-12-12
Prior Application removed - See File Wrappe
NUMBER OF SEQ ID NOS: 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ESULT 7
S-10-015-387A-275
Sequence 275, Application US/10015387A
Publication No. US20030135034A1
GENBRAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Botson. Dan 1.
APPLICANT: Eaton, Dan 1.
APPLICANT: Force, Wei-Qiang
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
PRIOR FILING DATE: 1998-10-22
PRIOR APPLICATION NUMBER: 60/10526
PRIOR FILING DATE: 1998-10-22
PRIOR APPLICATION NUMBER: 60/105693
PRIOR FILING DATE: 1998-10-26
PRIOR APPLICATION NUMBER: 60/105694
PRIOR FILING DATE: 1998-10-26
                                                                                                                  APPLICATION NUMBER: 60/105807
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Best Local Similarity
Matches 228; Conser
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S-10-015-387A-275
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LENGTH: 432
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US-10-063-735-112

Sequence 112, Application US/10063735

Publication No. US20330138982A1

GENERAL INFORMATION:
APPLICANT: Eaton, Dan L.
APPLICANT: Gendard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Granabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3230RLCI
CURRENT APPLICATION NUMBER: US/10/063,735
CURRENT APPLICATION NUMBER: US/10/063,735

CURRENT APPLICATION NUMBER: US/10/063,735

LENGTH: 432

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                                   319 LWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPEGGVDTC
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US-10-006-130A-275
; Sequence 275, Application US/10006130A
; Publication No. US20030148375A1
; GENBRAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan 1.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Forny, Sherman
; APPLICANT: Godard, Applicant: Godard, Parisin Godard, Paudrey
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430RICI
CURRENT APPLICATION NUMBER: US/10/199,672
CURRENT APPLICATION NUMBER: US/10/052,586
PRIOR APPLICATION NUMBER: 60/059263
PRIOR APPLICATION NUMBER: 60/059266
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-18
PRIOR PLING DATE: 1997-02-4
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-24
PRIOR FILING DATE: 1997-10-24
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PRIOR FILING DATE: 1997-10-24
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APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Pani, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2830P1C7
CURRENT APPLICATION NUMBER: US/10/006,130A
CURRENT FILING DATE: 2002-03-19
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 477
SEQ ID NO 275
LENGTH: 432
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   Austin L.
Kenneth J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen, Jian
Desnoyers, Luc
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Pan, James
Smith, Victoria
Watanabe, Colin K.
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Gurney, Austin L.
Hillan, Kenneth J
Pan, James
Paoni, Nicholas F
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ORGANISM: Homo
S-10-006-130A-275
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S-10-199-672-330
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PRIOR APPLICATION NUMBER: 60/063540
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063541
PRIOR FILING DATE: 1997-10-28
PRIOR PILING DATE: 1997-10-28
PRIOR PILING DATE: 1997-10-28
PRIOR FILING DATE: 1997-10-28
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 330
LENGTH: 432
LENGTH: A32
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Pred. No. 6.3e-117;
2; Mismatches 4;
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Sequence 275, Application US/10006172A;
Publication No. US20030153000A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Baten, David
APPLICANT: Baton, Dan 1.
APPLICANT: Ferrara, Napoleone
APPLICANT: Ferrara, Napoleone
APPLICANT: Gao, Wei-ciang
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APPLICANT: Gao, Wei-ciang
APPLICANT: Gaowski, Paul J.
APPLICANT: Gaowski, Paul J.
APPLICANT: Gaclowski, Paul J.
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Hillan, Kenneth J.
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APPLICANT: Pan, James
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Best Local Similarity 97.4%; Pre
Matches 228; Conservative 2;
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; ORGANISM: Homo Sapien
US-10-199-672-330
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NUMBER: 60/099536 1998-09-09 NUMBER: 60/099596 1998-09-09 NUMBER: 60/09598 1998-09-09 NUMBER: 60/09642 1998-09-09 NUMBER: 60/099642 1998-09-09 NUMBER: 60/099741 1998-09-10 NUMBER: 60/099763 NUMBER: 60/099763	100000000000000000000000000000000000000	1,10068 1,10068 1,10068 1,10071 1,10084 1,10084 1,10091 1,10101 1,10101 1,10107 1,10101 1,10101 1,10107 1,10107 1,10107 1,10101 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,10107 1,1010
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Bequance 330, Application US/10187749

Publication No. US20030153036A1

GENERAL INPORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Goddward, Paul J.
APPLICANT: Goddwark, Paul J.
APPLICANT: Goddwark, Paul J.
APPLICANT: Goddwark, Paul J.
APPLICANT: Goddwark, Paul J.
APPLICANT: Goddwark, Paul J.
APPLICANT: Wacanabb, Colin K.
APPLICANT: Walliam I.
APPLICANT: Wacanabb, Colin K.
APPLICANT: Matanabb, Colin K.
APPLICANT: Wacanabb, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Wacanabb, Colin K.
APPLICANT: Wacanabb, Colin K.
APPLICANT: Pan, Janes
APPLICANT: Wacanabb, Colin K.
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larity 97.4%; Pred. No. 6.3e-117;
Conservative 2; Mismatches 4;
PRIOR APPLICATION NUMBER: 60/105104
PRIOR FILING DATE: 1998-10-21
PRIOR APPLICATION NUMBER: 60/105169
PRIOR FILING DATE: 1998-10-22
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PRIOR APPLICATION NUMBER: 60/105882
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PRIOR FILING DATE: 1998-10-27
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US-10-194-457-330

Sequence 330, Application US/10194457

Publication No. US20030153037A1

GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
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APPLICANT: Wood William I.
APPLICANT: Wood William I.
APPLICANT: Anag. Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDES ENCODING THE SAME
TITLE OF INVENTION: ACIDES ENCODING THE SAME
TITLE OF INVENTION NUMBER: 10/05286
CURRENT APPLICATION NUMBER: 10/05286
FRIOR FILING DATE: 1997-09-18
FRIOR FILING DATE: 1997-09-18
FRIOR APPLICATION NUMBER: 60/062120
FRIOR PILING DATE: 1997-10-17
FRIOR APPLICATION NUMBER: 60/063120
FRIOR PILING DATE: 1997-10-24
FRIOR FILING DATE: 1997-10-27
FRIOR APPLICATION NUMBER: 60/063120
FRIOR PILING DATE: 1997-10-24
FRIOR PILING DATE: 1997-10-24
FRIOR PILING DATE: 1997-10-27
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FRIOR APPLICATION NUMBER: 60/063486

PRIOR FILING DATE: 1997-10-21

PRIOR APPLICATION NUMBER: 60/063540

PRIOR FILING DATE: 1997-10-28

PRIOR FILING DATE: 1997-10-28

PRIOR FILING DATE: 1997-10-28

PRIOR FILING DATE: 1997-10-28

PRIOR FILING DATE: 1997-10-28

Remaining Prior Application data removed - 8

NUMBER OF SEQ ID NOS: 612

LENGTH: 432
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US-10-187-749-330
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APPLICANT: Goddard, Audrey
APPLICANT: Goddwaki, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C194
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Pred. No. 6.3e-117;
2; Mismatches 4;
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PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063541
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063544
PRIOR FILING DATE: 1997-10-28
Prior Application data removed - See Fi
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 330
LENGTH: 432
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GENERAL INFORMATION:
APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
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NUMBER OF SEQ ID NOS: 612
SEQ ID NO 330
LENGTH: 432
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ORGANISM: Homo Sapien
S-10-184-642-330
                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo Sapien
S-10-194-457-330
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259 KLGSFPSLAVAKIIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFDEELTPATP
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199 RVVGGEEASVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHCFRKHTDVFNWKVRAGSD
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US-10-196-747-330
Sequence 330, Application US/10196747
Publication No. US20030162250A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gotowski, Paul J.
APPLICANT: Gotowski, Paul J.
APPLICANT: Gotowski, Paul J.
APPLICANT: Gotowski, Paul J.
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: AATON NUMBER I.
APPLICANT: TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION NUMBER: 2002-07-16
CURRENT APPLICATION NUMBER: 2002-07-16
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 330
LENGTH: 432
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US-10-196-747-330
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RESULT JX0172

coagulation factor	plasmin (EC 3.4.21	frypsin-related pr	membrane-bound ard	chymotrypsin (EC 3	trypsin (EC 3.4.21	plasmin (EC 3.4.21	trypsin (EC 3.4.21	enteropeptidase (E	enteropeptidase (E	trypsin (EC 3.4.21	trypsin (EC 3.4.21	plasmin (EC 3.4.21	enteropeptidase (E	plasmin (EC 3.4.21	trypsin-like prote
KFHU1	PLMS	S40004	JC7731	KYRTB	840005	A61545	I38363	A53663	A56318	TRDGC	A27547	PLHU	A43090	PLBO	TRWV5Y
τ-1	Н	0	N	Н	(1)	7	7	Н	Н	Н	0	Н	Н	Н	<b>,-</b> 4
625	812	274	855	263	275	455	259	1034	1019	246	247	810	1035	812	238
27.6	27.6	27.5	27.5	27.4	27.3	27.3	27.2	27.2	27.2	27.0	27.0	26.9	26.8	26.7	26.7
442	441.5	440	440	439	437	436	435.5	435.5	435	432.5	432	430.5	428.5	427.5	427

## ALIGNMENTS

```
hepsin (EC 3.4.21.-) - human
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 18-Jun-1999
C;Accession: S00845
R;Leytus, S.P.; Loeb, K.R.; Hagen, F.S.; Kurachi, K.; Davie, E.W.
Biochemistry 27, 1067-1074, 1988
A;Title: A novel trypsin-like serine protease (hepsin) with a putative transmembrane doma A;Reference number: S00845; MUID:88209431; PMID:2835076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50 DKIVGGYALDVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHCFRKHTDVFN-WKVRAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      221 AVAQASPHGLQLGVQAVVYHGGYLPFRDPNSEENSNDIALVHLSSPLPLTEYIQPVCLPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          221 GIPEGGVDICOGDSGGPLMYO ----SDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            109 SDKLGSFPSLAVAKIIIIEFNPMYP-----KDNDIALMKLQFPLTFSGTVRPICLPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         161 FDEELTPATPLWIIGWGFTKONGGKWSDILLOASVQVIDSTRCNADDAYOGEVTEKMMCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             281 AGQALVDGKICTVTGWGNT-QYYGQQAGVLQEARVPIISNDVCNGADFYGNQIKPKWFCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                     A;Accession: S00845
A;Molecule type: mRNA
A;Residues: 1-417 <LEY>
A;Cross-references: EMBL:X07732; NID:g32063; PIDN:CAA30558.1; PID:g32064
C;Genetics:
                                                                                                                                                                                                                                                                                                        A.Cross-references: EMBL:X07732; NID:g32063; PIDN:CAA30558.1; PID:g3206
C;Genetics:
A;Gene: GDB:HPN; TMPRSS1; hepsin
A;Cross-references: GDB:135685; OMIM:142440
A;Map position: 19q11-19q13.2
C;Superfamily: hepsin; trypsin homology
C;Keywords: hydrolase; liver; serine proteinase; transmembrane protein
F;23-45/Domain: trypsin homology <TRY>
F;163-400/Domain: trypsin homology <TRY>
F;188-204,291-359,322-338,349-381/Disulfide bonds: #status predicted
F;203,257,353/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                417;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 31.6%; Score 505.5; DB 1; Length Best Local Similarity 41.1%; Pred. No. 1.5e-37; Matches 101; Conservative 36; Mismatches 94; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             405
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RESULT
S00845
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Species: Mus musculus (house

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F;20-109/Domain: apple repeat <API>
F;110-199/Domain: apple repeat <API>
F;110-199/Domain: apple repeat <AP2>
F;200-289/Domain: apple repeat <AP3>
F;201-380/Domain: apple repeat <AP4>
F;291-380/Domain: apple repeat <AP4>
F;391-638/Product: plasma kallikrein light chain #status experimental <LCH>
F;391-621/Domain: trypsin homology <TRX>
F;21-104,47-77,51-57,111-194,137-166,141-147,201-284,227-256,231-237,292-375,318-347,322-F;127,215,308,396,494/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;434,483,578/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KIVGGYALDVDSWPWQVSIQY-----DKQHVCGGSILDPHWVLTAAHCFRKHTDVFNWK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----VRAGSDKLGSFP--SLAVAKIIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98 IVFGAQEIBYGRNKPVKEPQEERYVQKIVIHEKYNVVTEGNDIALLKVTPPVTCGNFIGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ICLPFFDEELTPATP - - LWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                               #status
                                                NID:949857; PIDN:CAA36704.1;
A; Residues: 1-418 <KLE>
A; Cross-references: GB:X52466; NID:g49857; PIDN:CAA36704.1
C; Superfamily: acrosin; trypsin homology
C; Keywords: glycoprotein; hydrolase; serine proteinase
F; 39-283/Domain: trypsin homology <TRY>
F; 18, 208/Binding site: carbohydrate (Asn) (covalent) #stat
F; 21-151/Disulfide bonds: #status predicted
F; 25-158/Disulfide bonds: #status predicted
F; 70-86/Disulfide bonds: #status predicted
F; 85, 139, 238/Active site: His, Asp, Ser #status predicted
F; 207-223/Disulfide bonds: #status predicted
F; 207-223/Disulfide bonds: #status predicted
F; 234-264/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2;
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Pred. No. 2e-36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        plasma kallikrein (EC 3.4.21.34) precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30.8%;
larity 41.5%;
Conservative 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 102; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of mouse proacrosin deduced from the cDNA sequence and its MUID:91185335; PMID:2127931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ';20-42/Product: acrosin light chain #status predicted <ALC>
';43-321/Product: acrosin heavy chain #status predicted <AHC>
';43-286/Domain: trypsin homology <TRY>
';22,211/Binding site: carbohydrate (Asn) (covalent) #status predicted
';25-155,29-162,74-90,178-247,210-226,237-267/Disulfide bonds: #status predicted
';89,143,241/Active site: His, Asp, Ser #status predicted
';235/Binding site: substrate (Asp) #status predicted
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37344
crosin (EC 3.4.21.10) precursor form 1 - mouse
575ecies: Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGGSILDPHWVLTAAHCFRKHTDVFNWK-----VRAGSDKLGSFP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 QQERYVQKIVIHEKYNVVTEGNDIALLKITPPVTCGNFIGPCCLPHF-KAGPPQIPHTCY
                                                                                                                                                                                                                                                                                                                                                                                                          PID:9238707
Y.; Arai, Y
                                                      pate: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 2; Accession: JX0172; JX0138
; Accession: JX0172; JX0138
; Watanabe, K.; Baba, T.; Kashiwabara, S.; Okamoto, A.; Arai, Y.
Biochem. 109, 828-833; 1991
; Title: Structure and organization of the mouse acrosin gene.
; Reference number: JX0172; MUID: 92041732; PMID: 1939002
; Accession: JX0172
; Molecule type: DNA
; Residues: 1-436 <WAT>
; Cross-references: GB: S66245; NID: g238706; PIDN: AAB20293.1; PID: ; Kashiwabara, S.; Baba, T.; Takada, M.; Watanabe, K.; Yano, Y.; Jitle: Primary structure of mouse proacrosin deduced from the circles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31.2%; Score 499; DB 2; Length 43 39.0%; Pred. No. 5.9e-37; ive 43; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            190/1; 238/3
trypsin homology
n; hydrolase; serine proteinase; sperm
equence #status predicted <SIG>
n light chain #status predicted <ALC>
in heavy chain #status predicted <AHC>
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crosomal protease
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Best Local Similarity 39.0 Matches 112; Conservative

Query Match

QY-----DKQHV

70

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ā

OIFTSHNSRRYH

61

SLA--VAKIIIIE

117

بخ ď 173

<u>≻</u>, ā |||||||| : : DSGGPLMCRDNVD

240

.;Reference number: A37344;

';Status: preliminary
';Molecule type: mRNA

DSGGPLMYQSD--

₹

Molecule type: mRNA; Residues: 4-436 <KAS>; Cross-references: GB:D0075; Comment: Acrosin is an acri-binding activity.

;Reference number: .; Accession: JX0138 .;Introns: 26/2; 95/2; 190, ;Superfamily: acrosin; try; ;Keywords: glycoprotein; ;1-19/Domain: signal sequ

'; Genetics:

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and light chair
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G.; Rougeon, R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hydrolase;
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11a, G.; Rougeon, F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: A39180; MULD:91129230; FMILD:1993180
A; Accession: A39180
A; Molecule type: DNA
A; Accession: A39180
A; Molecule type: DNA
A; Cross-references: GBR3-05315
A; Note: the authors translated the codon GAG for residue 81 as Gln
R; Seidah, N. G.; Ladenhelm, R.; Mbikay, M.; Hamelin, J.; Lutfalla, G.; Rougeon, DNA B; 56-574, 1989
A; Title: The CDNA structure of rat plasma kallikrein.
A; Reference number: A33320; MUID:90091743; PMID:2598771
A; Accession: A33320; MUID:90091743; PMID:2598771
A; Accession: A33320; MUID:90091743; PMID:2598771
A; Cross-references: GB:M30282; NID:G205010; PIDN:AAA41463.1; PID:G205011
A; Note: part of this sequence, including the amino ends of both the heavy and 1 R; Paquin, J.; Benjannet, S.; Sawyer, N.; Lazure, C.; Chretien, M.; Seidah, N.G. Biochim. Biophys: Acta 999; 103-110, 1989
A; Title: Rat plasma kallikrein: purification, NH(2)-terminal sequencing and dev A; Residues: 20-45;391-413 <PAC>
A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Mesidues: 20-45;391-413 <PAC>
A; Title: The cDNA structure of rat plasma kallikrein.
A; Meference number: 153041
                                                                                                      172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       plasma kallikrein (EC 3.4.21.34) precursor - rat
N;Alternate names: Fletcher factor; kininogenin; serum kallikrein
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1992 #sequence revision 30-Sep-1992 #text_change 18-Jun-1999
C;Accession: A39180; A33320; S06851; I53041; S06852
R;Beaubien, G.; Rosinski-Chupin, I.; Mattei, M.G.; Mbikay, M.; Chretien, M.;
Biochemistry 30, 1628-1635, 1991
A;Title: Gene structure and chromosomal localization of plasma kallikrein.
A;Reference number: A39180; MUID:91129236; PMID:1993180
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                                                                                                                                                                                                                                 SLA--VAKIIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFDEELTPATP--LW
                                                                                                                                                   QQERYVQKİVİHEKYNAVTEGNDİALLKVTPPVTCGDFVGPGCLPHF-KSGPPRIPHTCY
                                                                                                                                                                                                     IIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPEGGVDTCQG
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Keywords: blood coagulation; duplication; fibrinolysis; glycoprotein;
71-19/Domain: signal sequence #status predicted <SIG>
720-390/Product: plasma kallikrein heavy chain #status experimental <MA;20-109/Domain: apple repeat <API>
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;391-638/Product: plasma kallikrein light chain #status experimental
                                                                                                                                                                                                                                                                                                      276
                                                                                                                                                                                                                                                                                                    DSGGPLMYQSDQ---WHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWI
                                                                                                                                                                                                                                                                                                                                   tatus: translated from GB/EMBL/DDBJ
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                                                                                                                                                                                448 YGGILSLSEITKETPSSRIKELIIHQEYKVSEGNYDIALIKLOTPLNYTEFOKPICLPSK 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18407
crosin (EC 3.4.21.10) precursor - rat;
;Contains: proacrosin
;Species: Rattus norvegicus (Norway rat)
;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 22-Jun-1999
;Date: ---- c18407; S30037; A56620
                                                                                                                                                                                                                                                                                                                                                     276
                                                                                                                                               RAG----SDKLGSFPSLAVAKIIIIBFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFF
                                                                                                                                                                                                                                                                               SO8 ADTNTIXTNCWVTGWGYTKEQ-GETQNILQKATIPLVPNEEC--QKKYRDYVINKQMICA
                                                                                                                                                                                                                                                      GWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEK-MMCA
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                                                                                               IPWOVŚLOVKLVSQTHLCGGSIIGROWVLTAAHCFDGIPYPDV--WRI
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                                                                                                                                                                                                                                                                                                                                                                            )SGGPLMYQ-SDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWI
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Superfamily: acrosin, trypsin homology

Keywords: glycoprotein; hydrolase; serine proteinase; sperm;

1-19/Domain: signal sequence #status predicted <SIG>;

20-43/Domain: acrosin light chain #status predicted <LCH>;

44-437/Domain: acrosin homology <TRY>

22,211/Binding site: carbohydrate (Asn) (covalent) #status prints;

25-155,29-163/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Residues: 1-254, 'LCDR', 259, 'DHEL', 264, 'GRLC', 269-437 < KLE2>; Cross-references: EMBL:X59254; NID:g57282; PIDN:CAA41947.1; ; Kremling, H.; Flake, A.; Adham, I.M.; Radtke, J.; Engel, W. NA Seq. 2, 57-60, 1991
; Title: Exon-intron structure and nucleotide sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ure and nucleotide sequence of the MUID:92199245; PMID:1802037
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78-247/Disulfide bonds: #status predicted
0-226/Disulfide bonds: #status predicted
77-267/Disulfide bonds: #status predicted
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3.1e-36;
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77;
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ilarity 39.7%; Pred. No. 3.1e
Conservative 38; Mismatches
 Mismatches
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ita Library, April 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Accession: S18407; S30037; A56620; Klemm, U.; Flake, A.; Engel, W.; iochim. Biophys. Acta 1090, 270-272, Title: Rat sperm acrosin: cDNA seque; Reference number: S18407; WUID:92031
 41;
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                                              KIVGGYALDVDSW
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;Accession: A56620
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;Molecule type: mRNA
;Residues: 1-437 <KLE>
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; Molecule type: mRNA
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Binding site: carbohydrate (Asn) (covalent) #status predicted
ydrate (Asn) (covalent) #status experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.4.21.-) - rat
Rattus norvegicus (Norway rat)
----1995 #sequence_revision 06-Jan-1995 #text_change 18-Jun-1999
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                                                                                                                                                                   KIVGGYALDVDSWPWQVSIQ---YDKQHVCGGSILDPHWVLTAAHCFR--KHTDVFNWKV
                                                                                                                                                                                                                                  ---SDKLGSFPSLAVAKIIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFF
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Residues: 1-Fig. 1878.
Cross-references: EMBL:X70900; NID:g57928; PIDN:CAA50256.1; PID:g57929; Cross-references: EMBL:X70900; NID:g57928; PIDN:CAA50256.1; PID:g57929; Superfamily: hepsin; trypsin homology
Reywords: hydrolase; liver; serine proteinase; transmembrane protein ;22-44/Domain: transmembrane #status predicted <TWN>
162-399/Domain: trypsin homology <TRY>
187-203,290-358,321-337,348-380/Disulfide bonds: #status predicted;202,256,352/Active site: His, Asp, Ser #status predicted
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                                                                  His, Asp, Ser #status predicted
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3, 350-352, 1993
nce analysis of rat hepsin, a
; MUID:93305733; PMID:8318546
                                                                                                30.6%; Score 489; DB 1; L 42.2%; Pred. No. 7.4e-36; ive 45; Mismatches 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 479.5; DB 1;
Pred. No. 3.2e-35;
3; Mismatches 95;
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39.8%;
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Best Local Similarity 42.2
Matches 100; Conservative
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Best Local Similarity 39.88
Matches 98; Conservative
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;391-621/Domain: trypsin hc
;21-104,47-77,51-57,111-194
;127,215,308,453,459,494/Bi
;396/Binding site: carbohyc
;434,483,578/Active site: H
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;Status: preliminary
;Molecule type: mRNA
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plasma kallikrein (EC 3.4.21.34) precursor - human
NiAlternate names: kininogenin; plasma prekallikrein
C;Species: Homo sapiens (man)
C;Date: 13-Mug-1986 #sequence. Tevision 13-Aug-1986 #text_change 18-Jun-1999
C;Date: 13-Aug-1986 #sequence revision 13-Aug-1986 #text_change 18-Jun-1999
C;Date: 13-Aug-1986 #sequence revision 13-Aug-1986 #text_change 18-Jun-1999
R;Chung D.W.; Pujikkawa, K.; McMullen, B.A.; Davie, E.W.
Biochemistry 25, 2410-2417, 1986
A;Title: Human plasma prekallikrein, a zymogen to a serine protease that contains four te A;Recession: A00921; MUID:86243359; PMID:3521732
A;Reference number: A00921; MUID:919262; PIDN:AAA60153.1; PID:g190263
A;Residues: 1-638 cHUJ
A;Residues: 1-638 cHUJ
A;Residues: 1-638 cHUJ
A;Recession: A37939; MUID:91152016; PMID:1998666
A;Recession: A37939
A;Title: Location of the disulfide bonds in human plasma prekallikrein: the presence of 1
A;Recession: A37939
A;Recession: A37939
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A;Recession: A37
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Crosin (EC 3.4.21.10) precursor - pig
N;Alternate names: 53K fucose-binding protein
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A34170; S08994; S02428; S04940; S16657; S02780; S10695; S12968
C;Accession: A34170; Watanabe, K.; Itoh, H.; Michikawa, Y.; Kimura, K.; Takada, J. Biol. Chem. 264, 11920-11927, 1989
          R. Adham, I. M.; Klemm, U.; Maier, W.M.; Engel, W.

Hum. Genet. 84, 125-138, 1990
A;Title: Molecular cloning of human preproacrosin cDNA.
A;Reference number: A£1022
A;Status: not compared with conceptual translation
A;Molecula type: mRNA
A;Residues: not compared with conceptual translation
A;Molecula type: mRNA
A;Residues: 1.63, T', 65-225, V', 227-267, R', 269-421 <ADH>
A;Residues: 1.63, T', 75-225, V', 227-267, R', 269-421 <ADH>
A;Residues: 1.63, T', 75-225, V', 227-267, R', 269-421 <ADH>
A;Residues: 1.63, T', 75-225, V', 227-267, R', 269-421 <ADH>
A;Reference number: S03330, MUID:89153568; PMID:2493394
A;Reference number: S03330, MUID:89153568; PMID:2493394
A;Reference number: S03330, MUID:89153568; PMID:2493394
A;Reference number: S03320, MUID:89153568; PMID:2493394
A;Reference number: S03320, MUID:89153568; PMID:2493394
A;Reference signal.
A;References: GB:119645, OMIM:102480
A;References: GB:119645, OMIM:102480
A;References: GB:119645, OMIM:102480
A;References: GB:119645, OMIM:102480
A;References: GB:119645, OMIM:102480
A;References: GB:119642, 189/2; 23/3
C;Superfamily: acrosin light chain #status predicted <LGF>
F;20-421/Product: acrosin light chain #status predicted <LGF>
F;20-421/Product: acrosin light chain #status predicted <AGH>
F;20-421/Product: acrosin light chain #status predicted F;20-421/Product: acrosin light chain #status predicted F;20-421/Product: acrosin light chain #status predicted F;20-126/Disulfide bonds: #status predicted
F;20-420/Abisulfide bonds: #status predicted
F;20-225/Disulfide bonds: #status predicted
F;20-226/Disulfide bonds: #status predicted
F;20-226/Disulfide bonds: #status predicted
F;20-226/Disulfide bonds: #status predicted
F;20-226/Disulfide bonds: #status predicted
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6.6e-35;
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Best Local Similarity 41.0%; Pred. No. 6.66
Matches 100; Conservative 37; Mismatches
      W.M.;
      I.M.; Klemm, U.; Maier,
t. 84, 125-128, 1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ricoin (BC 3.4.21.10) precursor - human

Species: Homo sapiens (man)

Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 16-Jun-2000

Accession: S11674; S23499; S12063; A61022; S03330

*Keime, S.; Adham, I.M.; Engel, W.

ur. J. Biochem. 190, 195-200, 1990

;Title: Nucleotide sequence and exon-intron organization of the human proac; Reference number: S11674; MUID: 90306003; PMID: 2114285

Accession: S11674

;Molecule type: DNA

;Residues: 1-421 <KEI>
                                                           22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 214 TEKMMCAGIPEGGVDTCQGDSGGPLMYQ---SDQWHVVGIVSWGYGCGGPSTPGVYTKVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51 KIVGGYALDVDSWPWQVSIQY-----DKQHVCGGSILDPHWVLTAAHCFRKHTDVFNWK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIDN:CAA37964.1; PID:g1216165 for residue 64 as Thr and CTG J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          105 VRAGSDKL---GSFPSLA----VAKIIIIEFNPMYPKDNDIALMKLOFPLTFSGTVRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     156 ICLPFFDEELTPATP--LWIIGWGFTKQNGGKWSDILLQASVQVIDSTRCNADDAYQGEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     160 GCLPTF-RAGPPKIPQTCYVAGWGYIREKAPRPSPVLLEARVBLIDLDLCNSTQWYNGRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100 LVFGAEEIEYGNKFVRAPLQERYVEKIVIHEKYNIVNEGNDIALLKITPPVSCGPFIGP
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                               (guinea pig)
Ge_revision 10-Nov-1995 #text_change
                                                                                                                                                                    proacrosin
                                                                                                                                                                                                                Accession: $29599
Molecule type: mRNA
;Residues: 1-421 <GER>
;Cross-references: EMBL:Z12153; NID:g49559; PIDN:CAA78137.1;
;Superfamily: acrosin; trypsin homology
;Keywords: glycoprotein; hydrolase; serine proteinase
;41-284/Domain: trypsin homology <TRY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
crosin (EC 3.4.21.10) precursor - guinea pig (fragment)
;Species: Cavia porcellus (guinea pig)
;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    restriction
PMID:1628652
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Pred. No. 3.9e-35;
42; Mismatches 85;
                                                                                                                                                                      pig
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of guinea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vazquez-Levin, M.H.; Reventos, J.; Gordon, r. J. Biochem. 207, 23-26, 1992; Title: Molecular cloning, sequencing and re;Reference number: S23499; MUID:92331659; PP;Accession: S23499; Accession: S23499; Accession: S23499
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May
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id sequence
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Cross-references: EMBL:M77378
Note: the nucleotide sequence was
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Best Local Similarity 39.89
Matches 98; Conservative
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;Reference number: $12063
;Accession: $12063
;Molecule type: DNA
;Residues: 1-225,'R',227-421
                                                                            Accession: $29599
Gerton, G.L.; Hoff, H.B.;
ubmitted to the EMBL Data 1
;Description: The amino ac;
Reference number: $29599
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279 DYLDWI
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us-09-607-745-9.rpr

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LYDOLOGY (EC 3.4.21.4) precursor - mouse C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 22-Jun-1989
C; Accession: B25528
R; Stevenson, B.J.; Hagenbuechle, O.; Wellauer, P.K.
Nucleic Acids Res. 14, 8307-8330, 1986
A; Title: Sequence organisation and transcriptional regulation of the mouse elasta A; Reference number: A93646; MUID:87066713; PMID:3641189
A; Reference number: A93646; MUID:87066713; PMID:3641189
A; Accession: B25528
A; Molecule type: mRNA
A; Residues: 1-246 cSTE>
A; Coss-references: GB:X04574; NID:954918; PIDN:CAA28243.1; PID:954919
C; Superfamily: trypsin; trypsin homology
C; Superfamily: trypsin; trypsin homology
C; Reywords: calcium binding; hydrolase; predicted <81G>
F; 24-246/Product: trypsin #status predicted <AMT>
F; 24-239/Domain: signal sequence #status predicted <AMT>
F; 24-239/Domain: trypsin homology <TRY>
F; 24-239/Domain: trypsin homology of TRY>
F; 24-239/Domain: trypsin homology ser #status predicted
F; 30-160, 48-64, 132-233, 139-206, 171-185/Disulfide bonds: #status predicted
F; 77, 80, 85/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --DKQHVCGGSILDPHWVLTAAHCFRKHTDVFNWK 104
                                                                                                                       VRAGSDKL--GS----FPSLA---VAKIIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRP
                                                                                                                                                                                                                                                                      159 GCLPQF-KAGPPRAPQTCWVTGWGYLKEKGPRTSPTLQEARVALIDLELCNSTRWYNGRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TEKMMCAGIPEGGVDTCQGDSGGPLMYQ---SDQWHVVGIVSWGYGCGGPSTPGVYTKVS
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                                                                        51 KIVGGYALDVDSWPWQVSIQY-
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     102;
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;Molecule type: mRNA
;Residues: 1-7,9-210,'Q',212-216,'VT',219-346,'A',348-388,390-393,'GN',396,'LVE',399-40
;Cross-references: EMBL:X14844
;Note: the authors translated the codon CCT for residue 240 as Ala, GCC for residue 264
dedud
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Tosin homology
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                                                                                                                                                                                                                                                                                                                                         partial
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ubmitted to the EMBL Data Library, March 1989

;Reference number: $16657

;Accession: $16657

;Accession: $16657

;Accession: $16657

;Molecule type: mRNA
;Residues: 1-7,9-210,'Q',212-216,'VT',219-346,'A',348-388,390-398,'KELL' <AD2
;Cross-references: EMBL:X14844; NID:g1867; PIDN:CAA32948.1; PID:g1868
;Note: the difference at the carboxyl end is due to a frameshift error
;Baba, T.; Michikawa, Y.; Kawakura, K.; Arai, Y.
EBS Lett. 244, 132-136, 1989
;Title: Activation of boar proacrosin is effected by processing at both N- a
;Reference number: $02780; MUID:89171246; PMID:2494060
;Accession: $02780
;Molecule type: protein
;Residues: 17-69 <BA2>
;Toepfer-Petersen, E.; Steinberger, M.; von Eschenbach, C.E.; Zucker, A.
EBS Lett. 265, 51-54, 1990
;Title: Zona pellucida-binding of boar sperm acrosin is associated with the
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jol. Chem. Hoppe-Seyler 371, 317-323, 1990
; Title: Is sperminogen a modified proacrosin? Isolation, purification, Reference number: S08994; MUID:90253655; PMID:2111146
; Accession: S08994
; Molecule type: protein
; Residues: 'X', 18, 'X', 20-25, 'X', 27-32, 'X', 34-38, 'X', 40-50 cCEC>
; Toepfer-Petersen, E.; Henschen, A.
EBS Lett. 226, 38-42, 1987
; Title: Acrossin shows zona and fucose binding, novel properties for a segment of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the
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        zymogen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tsaousidou,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    473.5; DB 1; Length 415; No. 1.1e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and fucose binding, novel properties MUID:88083633; PMID:3480243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Accession: S02428
;Molecule type: protein
;Residues: 17-32;40-55 <TOE>
;Adham, I.M.; Klemm, U.; Maier, W.M.; Hoyer-Fender, S.; Tsaousi
ur. J. Biochem. 182, 563-568, 1989
;Title: Molecular cloning of preproacrosin and analysis of its
;Reference number: S04940; MUID:89325301; PMID:2502391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ď
  sms of boar acrosin
PMID:2745422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29.6%; Score 41.5%; Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;40-415/Product: acrosin heavy (B) cha;40-283/Domain: trypsin homology <TRY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;Reference number: S10695; N;Accession: S10695
;Molecule type: protein
;Residues: 40-62 <TO2>
;Toepfer-Petersen, E.; Calve
EBS Lett. 275, 139-142, 1990
;Title: Complete localizatio
  and mate
A34170;
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Accession: $12968;
Molecule type: protein;
Residues: 17-29;34-66;68-;
Superfamily: acrosin; try
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Reference number: S02428;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                      ;Accession: A34170
;Status: preliminary
;Molecule type: mRNA
;Residues: 1-415 <BAB>
        Activation
                                   Reference number:
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elastase

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125
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                                                                                                                                                                                                                                                                                                                                                                        126 IEFNPMYPK---DNDIALMKLQFPLTFSGTVRPICLPFFDEELTPA-TPLWIIGWGFTKQ
                                                                                                                                                                                                                                                                                                                                                                                                            --RHPNYNSWTLDNDIMLIKLASPVTLNARVASVPLP---SSCAPAGTQCLISGWGNTLS
                                                                                                                                                                ---GAAVAFPVDDDDKIVGGYTCRESSVPYQVSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPEGGVDTCQGDSGGPLMYQ
                                                                                                                               10 SRLLLLLVVSNLLLCQGVVSDYKDDDDVDAAALAAPFDDDDKIVGGYALDVDSWPWQVSI
                                                                                                                                                                                                                                                  QYDKQHVCGGSILDPHWVLTAAHCFRKHTDVFNWKVRAGSDKL----GSFPSLAVAKIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --SYPGDITHNMICVGFLEGGKDSCQGDSGGPVVCN
                                                                                                                                                                                                                                                                                        NAG-YHFCGGSLINDQWVVSAAHCYK----YRIQVRLGBHNINVLEGNEQFVDSAKI
           Length
                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      242 SDOWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYN 278
Query Match 29.4%; Score 470.5; DB 2; Best Local Similarity 40.1%; Pred. No. 1.1e-34; Matches 111; Conservative 35; Mismatches 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GE---LQGIVSWGYGCAQPDAPGVYTKVCNYVDWION
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RESULT T30337

276

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trypsin (EC 3.4.21.4) II precursor [validated] - human
NyAlternate names: trypsin 2; trypsin, anionic; trypsinogen II
C;Species: Homo sapiens (man)
C;Date: 03-Mar-1994 #sequence revision 03-Mar-1994 #text_change 08-Dec-2000
C;Accession: B2882; A61066; E43988
R;Emi, M.; Nakamura, Y.; Ogawa, M.; Yamamoto, T.; Nishide, T.; Mori, T.; Matsubara, K.
Gene 41, 305-310, 1986
A;Fitle: Cloning, characterization and nucleotide sequences of two cDNAs encoding human I
A;Reference number: A31544; MUD:86221712; PMD:3011602
A;Accession: B2882
A;Molecule type: mRNA
A;Residues: 1-247 <man
A;Residues: 1-247 <man
A;Residues: 1-247 <man
A;Reference number: A61066; MUD:90091010; PMD:2598466
A;Fitle: Immunoreactive anionic and cationic trypsin in human serum.
A;Reference number: A61066
A;Molecule type: protein
A;Residues: 16-39, X, 41-42, XXXXX, 47-49 <max
A;Residues: 16-39, X, 41-42, XXXXXX, 47-49 <max
A;Residues: 16-39, X, 41-42, XXXXX, 41-49 <max
A;Residues: 16-39, X, 41-42, XXXXX, 41-49 <max
A;Residues: 16-39, X, 41-42, XXXXX, 41-49 <max
A;Residues: 16-39, X, 41-42, XXXXX, 41-49 <max
A;Residues: 16-39, X, 41-42, XXXXX, 41-49 <max
A;Residues: 16-39, X, 41-42, XXXXX, 41-49 <max
A;Residues: 16-39, X, 41-42, XXXXX, 41-49 <max
A;Residues: 16-39, X, 41-42, XXXXX, 41-49 <max
A;Residues: 16-39, X, 41-42, XXXXX, 41-49 <max
A;Residues: 16-39, X, 41-42, XXXX, 41-49 <max
A;Residues: 16-39, X, 41-42, XXXX, 41-49 <max
A;Residues: 16-39, X, 41-42, XXXX, 41-49 <max
A;Residues: 16-39, X, 41-42,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and nucleotide sequences of two cDNAs encoding human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      on; serine proteinase; zymogen
<SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pseudogenes,
                                      SNGHRVVGGFQIDVSDAPYQVSLQYFNSHRCGGSVLDNKWVLTAAHC-TQGLDPSSLAVR
      DDDDKIVGGYALDVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHCFRKHTDVFNWKVR
                                                                                                                       AGSDKLGSFPSLAVAKIIIIEFNPMYPK---DNDIALMKLQFPLTFSGTVRPICLPFFDE
                                                                                                                                                           164 ELTPATPLWIIGWGFTKONGGKMSDILLQASVQVIDSTRCNADDAYQ--GEVTEKMMCAG
                                                                                                                                                                                                                                                                        SILDPHWVLTAAHCFRKHTDV----FNWKVRAGSDKLGSFPSLAVAKIIIIEFNPMYPK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 NLLLCQGVVSDYKDDDDVDAAALAAPFDDDDKIVGGYALDVDSWPWQVSIQYDKQHVCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --AAAVAAPFDDDDKIVGGYICEENSVPYQVSLN-SGYHFCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #status predicted
                                                                                                                                                                                                                                                                                                                                                    222 IPEGGVDTCQCDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWI
                                                                                                                                                                                                                                                                                                                                                                                           YQQGGKDACQGDSGGPLVADG---KLVGVVSWGYGCAQPGYPGVYGRVASVRDWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: GDB:PRSS2; TRY2
A;Cross-references: GDB:335289; OMIM:601564
A;Map position: 7q35-7q35
A;Note: the human genome contains at least ten trypsin genes or pseud C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; pancreas; protein digestion; serine proteinase F;1-15/Domain: signal sequence #status predicted <SIG>F;16-246/Product: trypsinogen II #status experimental <ZVM>F;16-23/Domain: activation peptide #status experimental <APT>F;24-246/Product: trypsin II #status predicted <BNZ>F;24-239/Domain: trypsin homology <TRY>F;24-239/Domain: trypsin homology <TRY>F;30-160,48-64,171-185,196-220/Disulfide bonds: #status predicted F;63,107,200/Active site: His, Asp, Ser #status predicted F;75,77,80,85/Binding site: calcium (Glu, Asn, Val, Glu) #status pred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .8e-34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29.0%; Score 464.5; 40.9%; Pred. No. 3.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Experimental source: mucinous ovarian tumor C, Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: protein A; Residues: 16-49 < KOI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 NLLLILTFV-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: B43988
                                                                                                                                                                             105
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Matches 11
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                                                                                                                                                                                                                                                                                                                                                    PIDN: AAC24717.1
                  Species: Xenopus laevis (African clawed frog)
;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 03-Feb-2003
;Accession: T30337
;Yang, J.C.; Lindsay, L.L.; Hedrick, J.L.
ubmitted to the EMBL Data Library, March 1998
;Description: cDNA cloning of ovochymase, a chymotrypsin-like protease rele;Reference number: Z20829
;Accession: T30337
;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in gene family in Anopheles gambiae are induced MUID:93327779; PMID:8335004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PWQVSIQYDKQHVCGGSILDPHWVLTAAHCFRKHTDVFNWKVRAGS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 110 DKLGSFPSLAVAKIIIIEFNPMYPK---DNDIALMKLQFPLTFSGTVRPICLPFFDEELT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PATPLWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPEG~
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    760 EKDACQGDSGGPLVCQNEKEQFSIYGLVSWGEGCGRVSKPGVYTKVRLFFTWIQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MYQS--DQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1524;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rypsin (EC 3.4.21.4) 2 precursor - African malaria mosquito ;Species: Anopheles gambiae (African malaria mosquito);Jate: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change;Accession: S35340; S40008; S35413
;Mueller, H.M.; Crampton, J.M.; della Torre, A.; Sinden, R.; Cr. MBO J. 12, 2891-2900, 1993
;Title: Members of a trypsin gene family in Anopheles gambiae a;Reference number: S35339; MUID:93327779; PMID:8335004
;Accession: S35340
;Molecule type: DNA
;Residues: 1-277 <MUE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87; Indels
                                                                                                                                                                                                                                                                              Molecule type: mRNA
Residues: 1-1524 <YAN>
Cross-references: EMBL:U81290; NID:g2981640; PID:g2981641;
Superfamily: tryosin related polyprotein; trypsin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Reference number: $40003
Accession: $40008
Molecule type: DNA
Residues: 1-277 <MU2>
Superfamily: trypsin; trypsin homology
Keywords: hydrolase; protein digestion; serine proteinase;
1-19/Domain: signal sequence #status predicted <SIG>
120-50/Domain: activation peptide #status predicted <APT>
51-27/Product: trypsin 2 #status predicted <APT>
61-27/Product: trypsin 2 #status predicted <APT>
61-27/Product: trypsin homology <TRY>
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                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 470; DB 2;
; Pred. No. 1.1e-33;
37; Mismatches 87
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Matches 101; Conservative
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- 2003
GenCore (c) 1993
        Copyright
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; Search time 11.2462 Seconds
(without alignments)
1221.015 Million cell updates/sec 2003, 07:39:05 November 23 un on:

US-09-607-745-9 1600 1 MDSKGSSQKSRLLLLLLVVSN......LNWIYNVWKAELSRHHHHHH 292

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ost-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

41:\* SwissProt atabase :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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### ALIGNMENTS

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SEQUENCE FROM N.A.

TISSUE=Pancreas;

X FIGURE=22388257; PubMed=12477932;

X Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peterrs G.J., Abramson R.D., Mullahy S.J.,

A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gibbs R.A.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gibbs R.A.,

A Halton D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

A Mitting M., Madan J.W., Green E.D., Dickson M.C.,

B Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

B Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

R "Generation and initial analysis of more than 15,000 full-length

Proc. Math Acad S. 17 R. 17 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 R. 18 
                         TMS4 HUMAN STANDARD; PRT; 437 AA.
Q9NRS4; Q9NZA5;
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
Transmembrane protease, serine 4 (EC 3.4.21.-) (Membrane-type serine protease 2) (MT-SP2).
TMPRSS4 OR TMPRSS3.
                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Pancreatic carcinoma;
MEDLINE=20283276; PubMed=10825129;
Wallrapp C., Haehnel S., Mueller-Pillasch F., Burghardt B.,
Iwamura T., Ruthenbuerger M., Lerch M.M., Adler G., Gress T.M.;
"A novel transmembrane serine protease (TMPRSS3) overexpressed in pancreatic cancer.";
Cancer Res. 60:2602-2606(2000).
                                                                                                                                                                                                                                                                                                Vertebrata; Euteleostomi;
i; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Smeekens S.S., Lorimer D.D., Wang E., Hou J., Linnevers C.,
"MT-SP2, a novel type II membrane serine protease expressed in
trachea, colon, and small intestine: identification, cloning, a
chromosomal localization.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . Natl. Acad. Sci. U.S.A. 99:16899-16903(2002). FUNCTION: MAY PLAY A ROLE IN TUMOR PROGRESSION, METASTASIS FORMATION AND TUMOR INVASION.
                                                                                                                                                                                                                                                                                              Craniata; Ve
Catarrhini;
                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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TMS4_HUMAN
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Query Match

Query Match

Query Match

Best Local Similarity 97.4%; Pred. No. 5.5e-111;

Matches 228; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

S1 KIVGGYALDVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHCFRKHTDVFNWKVRAGSD 110
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SEQUENCE OF 187-206, AND CHARACTERIZATION.

MEDLINE=97224034; PubMed=9070615;
Yasuoka S., Ohnishi T., Kawano S., Tsuchihashi S., Ogawara M.,
Masuda K.-I., Yamaoka K., Takahashi M., Sano T.;
Masuda K.-I., Yamaoka K., Takahashi M., Sano T.;
Trypsin-like protease found in the human airway.";
Am. J. Respir. Cell Mol. Biol. 16:300-308(1997).

-I-FUNCTION: May play some biological role in the host defense system on the mucous membrane independently of or in cooperation with other substances in airway mucous or bronchial secretions.

-I-CATALYTIC ACTIVITY: Preferentially cleaves the C-terminal side of arginine residues at the Pl position of certain peptides, cleaving Boc-Phe-Ser-Arg-4-methylcoumaryl-7-amide most efficiently and having an optimum pH of 8.6 with this substrate.

-I-ENZYME REGULATION: Strongly inhibited by diisopropyl fluorophosphate, leupeptin, antipain, aprotinin, and soybean trypsin inhibitor at 10 microm.

-I-SUBUNIT: Monomer.

-I-SUBUNIT: MONOMER.

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                                                                                                                                                                                                                                                                                                                                                                383
204 RVVGGEBASVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHCFRKHTDVFNWKVRAGSD 263
                                                                                                                                                                                                                                                                                                                                                          324 LWIIGWGFTKONGGKWSDILLOASVOVIDSTRCNADDAYOGEVTEKMMCAGIPEGGVDTC
                                                                                                                            KLGSFPSLAVAKIIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFDEELTPATP
                                                                                                                                                                     264 KLGSFPSLAVAKIIIIEFNPMYPKDNDIALMKLQFPLIFSGTVRPICLPFFDEELTPATP
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TISSUE SPECIFICITY: Located in the cells of the submucosal serous glands of the bronchi and trachea.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
SIMILARITY: Contains 1 SEA domain.
                                                                                                                                                                                                                                                                                        LWIIGWGFTKONGGKMSDILLOASVOVIDSTRCNADDAYOGEVTEKMMCAGIPEGGVDTC
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J. Biol. Chem. 273:11895-11901(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                 QGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         384 QGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Airway trypsin-like protease precursor (EC 3.4.21.-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=98234382; PubMed=9565616;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AVAKIIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFDEELT 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IST--TFPKLRMRVRNILIHNMYKSATHENDIALVRLENSVTFTKDIHSVCLPAATONIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PATPLWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPEGG
                                                                                                                                                                                                                                                                                                                                                                             CHAIN.
CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                              AIRWAY TRYPSIN-LIKE PROTEASE, NON-
CATALYTIC CHAIN.
AIRWAY TRYPSIN-LIKE PROTEASE, CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SERINE PROTEASE.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
AW; F4BCIDBO2OCFBBDO CRC64;
                                                                                                                                                                                                                                    Chordata; Craniata; Vertebrata; Buteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 418;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79; Indels
MEROPS; S01.301; -.

MIM; 605369; -.

GO; GO:0005576; C:extracellular; TAS.

GO; GO:000587; C:integral to plasma membrane; TAS.

GO; GO:0008233; F:peptidase activity; TAS.

GO; GO:0008233; F:peptidase activity; TAS.

GO; GO:000823; F:peptidase activity; TAS.

GO; GO:0007585; P:respiratory gaseous exchange; TAS.

InterPro; IPR001314; Chymotrypsin.

InterPro; IPR00134; SEA, 1.

Pfam; PF01390; SEA, 1.

Pfam; PF00089; trypsin; 1.

Pfam; PR00125; CHYMOTRYPSIN.

SMART; SM00200; SEA; 1.

PROSITE; PS50024; SEA; 1.

PROSITE; PS500134; TRYPSIN DOM; 1.

PROSITE; PS00134; TRYPSIN HIS; 1.

Hydrolase; Serine protease; Transmembrane; Signal-ancho Glycoprotein.

MINGOLOGIE: PS00135; TRYPSIN SER; 1.

Hydrolase; Serine Protease; Transmembrane; Signal-ancho Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL).

EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Transmembrane protease, serine 3 (EC 3.4.21.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32.9%; Score 526.5; DB 1
41.8%; Pred. No. 9.6e-42;
live 49; Mismatches 75
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Eukaryota, Metazoa,
Mammalia, Eutheria;
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ACT SITE
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MS3 MOUSE
D TMS3 MC
C Q8K1T0
I 15-SEP
I 15-SEP
I 15-SEP
E Transm
N TMPRSS
S MUS mu
C Eukary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AJ429216; CAD22137.1; -.

REMEL; AJ429216; CAD22137.1; -.

REMEL; AJ400738; CAC83350.1; -.

RESP; PO0761; LAN1.

RESP; PO0761; LAN1.

RESP; PO0761; LAN1.

RESP; PO0761; LAN1.

RESP; PO0761; LAN1.

RESP; PRO01254; Ser_protease_Try.

REPRO01254; Ser_protease_Try.

REAM; PRO089; Lrypsin, 1.

REAM; PRO089; Lrypsin, 1.

REAM; SMART; SM00120; LDLa; 1.

REAM; SMART; SM00120; LDLa; 1.

RESPS; RESPS; RESP; RESP; RESP; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RESPS; RES
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SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
                                                                                             Guipponi M., Vuagniaux G., Wattenhofer M., Shibuya K., Vazquez M., Dougherty L., Scamuffa N., Guida E., Okui M., Rossier C., Hancock M., Buchet K., Reymond A., Hummler E., Marzella P.L., Kudoh J., Shimizu N., Scott H.S., Antonarakis S.E., Rossier B.C.; "The transmembrane serine protease (TMPRSS3) mutated in deafness DFNB8/10 activates the epithelial sodium channel (ENaC) in vitro."; Hum. Mol. Genet. 11:2829-2836(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- TISSUE SPECIFICITY: Expressed in the spiral ganglion, the cells supporting the organ of Corti and the stria vascularis.
-!- PIM: Undegoes autoproteolytic activation.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
-!- SIMILARITY: Contains 1 SRCR domain.
-!- SIMILARITY: Contains 1 LDL-receptor class A domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY).
SIMILARITY).
SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBCELLULAR LOCATION: Type II membrane protein. Endoplasmic
SEQUENCE FROM N.A., SUBCELLULAR LOCATION, AND FUNCTION IN ENAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL)
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SERINE PROTEASE.
CHARGE RELAY SYSTEM (ECHARGE Y.)
BY SIMILARITY.
BY SIMILARITY.
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                                                                        PubMed=12393794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     reticulum.
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                                                                                                                                             51 KIVGGYALDVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHCFRKHTDVFNWKVRAGSD 110
                                                                                                                                                                                                                                                                                               391
                                                                                                                                                              111 KL--GSFPSLAVAKIIIIEFNPMY-PK--DNDIALMKLOFPLTFSGTVRPICLPFFDEEL
                                                                                                                                                                                                                       AT-EDGGDASPVLNHAAVPLISNKICNHRDVYGGIISPSMLCAGYLKG
                                                                                                                                                                                                                                                                FTKONGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPEG
                                                                                                                                                                                                                                                                                                                                       MYQSDQ-WHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nordata; Craniata; Vertebrata; Euteleostomi;
odentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                    10;
 BY SIMILARITY.

N-LINKED (GLCNAC. . .) (POTENTIAL)

L -> H (IN REF. 1; CAC83350).

V -> I (IN REF. 1; CAC83350).

; lABCBF10AF6E1EF6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Brain,
Mitsui S., Yamaguchi N.;
Mitsui S., Yamaguchi N.;
"Molecular cloning of mouse type 4 spinesin.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
-!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=4;
Name=4;
                                                                                         Length 453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Spinesin)
                                                                                                                    83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Brain;
Mitsui S., Yamaguchi N.;
"cDNA cloning of mouse spinesin.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 005398;
                                                                                    32.7%; Score 523; DB 1;
44.2%; Pred. No. 2.3e-41;
ive 41; Mismatches 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence=VSP_005397, VSP_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IsoId=Q9ER04-4; Sequence=VSP 005396;
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1
SIMILARITY: Contains 1 SRCR domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence=VSP_005395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence=Displayed;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FROM N.A. (ISOFORM 4)
                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                       ESULT 4

MS5 MOUSE

D TMS5 MOUSE
C Q9ER04; Q9ER02; Q9ER03;
T 16-OCT-2001 (Rel. 40, Cr
T 16-OCT-2001 (Rel. 40, La
T 28-FEB-2003 (Rel. 41, La
E Transmembrane protease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Cho
Mammalia; Eutheria; Rod
NCBI_TaxID=10090;
                                                                                     Query Match
Best Local Similarity
Matches 106; Conservat:
                                                                                                                                                                                                                                                                                                                      GVDTCQGDSGGPI
    TPATPLWIIGWG
                                                                                                                                                                                                                                                                                                                                      SLMDSPVPSHLV
                                                                                                                                                                                                                                                                                           PDGKLCWTSGWG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=Q9ER04-2;
   396
221
117
246
453 AA;
DISULFID
CARBOHYD
CONFLICT
CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    222 IPEGGVDTCQGDSGGPLMYQS-DQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYN 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           108 GSDKLGS---FPSLAVAKIIIIEFNPMYPKDN---DIALMKLQFPLTFSGTVRPICLPFF
                                                                                                                                                                                                                                                                                                                                                             Hydrolass; Seline process.

Glycoprotein; Alternative splicing.

DOMAIN 1 49 CYTOPLASMIC (POTENTIAL).

TO SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              276 GLVSHGAVRQHQGTMVEKIIP---HPLYSAQNHDYDVALLQLRTFINFSDTVDAVCLPAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEELTPATPLWIIGWGFTKONGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            333 BQYFPWGSQCWVSGWGHTDPSHTHSSDTLQDTMVPLLSTHLCNSSCMYSGALTHRMLCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Missing (in isoform 1).

/FTId=VSP 005397.

GGLVEEAWKP -> MEAQVGLLWV (in isoform / FTId=VSP 005398.

D -> G (IN REF. 1; BAB20277).

5CFC31789C6899AA CRC64;
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(BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                     Transmembrane; Signal-anchor;
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EXTRACELLULAR (POTENTIAL)
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InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR001190; Srcr_receptor.
Pfam; PF00089; trypsin; 1.
SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN HIS; 1.
PROSITE; PS00420; SRCR_1; FALSE_NEG.
PROSITE; PS00420; SRCR_1; FALSE_NEG.
PROSITE; PS50287; SRCR_2; 1.
Hydrolase; Serine protease; Transmembr
                   EMBL; AB016229; BAB20276.1; -
EMBL; AB016230; BAB20277.1; -
EMBL; AB016423; BAB20277.1; -
EMBL; AB041037; BAB40328.1; -
HSSP; P00763; 1DPO.
MEROPS; S01.313; -
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455 AA;
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RESULT 5 TMS3\_HUMAN

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454

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80:124-131 (2002)

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SEQUENCE FROM N.A. (ISOFORMS A AND T).

SEQUENCE FROM N.A. (ISOFORMS A AND T).

TISSUE=Ovarian carcinoma;

MEDLINE=20521358; PubMed=11068177;

Underwood L.J., Shigemasa K., Tanimoto H., Beard J.B., Schneider E.N.,

Wang Y., Parmley T.H., O'Brien T.J.;

"Ovarian tumor cells express a novel multi-domain cell surface serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WEDLINE=21904597; PubMed=11907649; MEDLINE=21904597; PubMed=11907649; Wattenhofer M., Di Iorio V., Rabionet R., Dougherty L., Pampanos A., Schwede T., Montserrat-Sentis B., Arbones L., Iliades T., Pasquadibisceglie A., D'Amelio M., Alwan S., Rossier C., Dahl H.-H.M., Petersen M.B., Estivill X., Gasparini P., Scott H.S.,
                                                             Last sequence update)
Last annotation update)
e, serine 3 (EC 3.4.21.-) (Serine protease
iated differentially-expressed gene-12 protein)
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ILE-53; SER-111 AND VAL-253.

MEDLINE=21317610; PubMed=11424922;

Ben-Yosef T., Wattenhofer M., Riazuddin S., Ahmed Z.M., Scott H.S., Kudoh J., Shibuya K., Antonarakis S.E., Bonne-Tamir B., Radhakrishna U., Naz S., Ahmed Z., Riazuddin S., Pandya A., Radhakrishna U., Naz S., Ahmed Z., Riazuddin S., Pandya A., Nance W.E., Wilcox B.R., Friedman T.B., Morell R.J.;

"Novel mutations of TMPRSS3 in four DFNB8/B10 families segregating "Novel mutations of TMPRS3 in four DFNB8/B10 families
                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20578749; PubMed=11137999;
MEDLINE=20578749; PubMed=11137999;
MEDLINE=20578749; PubMed=11137999;
MEDLINE=20578749; PubMed=11137999;
SCOLT H.S., Kudoh J., Wattenhofer M., Shibuya K., Berry A., Chrast Scott H.S., Mehdi S.Q., Radhakrishna U., Papasavvas M.P., Gehrig C., Younus F., Mehdi S.Q., Radhakrishna U., Papasavvas M.P., Gehrig C., Rossier C., Korostishevsky M., Gal A., Shimizu N., Bonne-Tamir B., Antonarakis S.E.;
"Insertion of beta-satellite repeats identifies a transmembrane protease causing both congenital and childhood onset autosomal recessive deafness.";
Nat. Genet. 27:59-63(2001).
                                                                                                                                                                                          Craniata, Vertebrata; Buteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cause of childhood
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MEDLINE=21354482; PubMed=11462234;
Masmoudi S., Antonarakis S.E., Schwede T., Ghorbel A.M., Grapapasavas M.P., Drira M., Elgaied-Boulila A., Wattenhofer Pappasavas M.P., Ayadi H., Guipponi M.;
Rossier C., Scott H.S., Ayadi H., Guipponi M.;
"Novel missense mutations of TMPRSS3 in two consanguineous families with non-syndromic autosomal recessive deafness.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SS3 gene are a rare caus
in Caucasian patients.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [5]
VARIANTS DFBN8/DFNB10 TRP-10
                                                                                                                      TADG-12) (Tumor associated
TMPRSS3 OR TADG12 OR ECHOS1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Petersen M.B., Estivill X. Antonarakis S.E.; "Mutations in the TMPRSS3 nonsyndromic deafness in C
                       P57727;
16-OCT-2001 (Rel. 40, C)
16-OCT-2001 (Rel. 40, Li
15-SEP-2003 (Rel. 42, Li
Transmembrane protease,
                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Cho:
Mammalia; Eutheria; Prir
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                     protease.";
Biochim. Biophys. Acta
НАРРРУИСТИНТРРУИСТИНТРРУИСТИНТРРУИСТИНТРРУИСТИННРРРУИСТИНТРРУИСТИНТРУИСТИНТРУИСТИНТИНТИ
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Gratri M

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                          PTM: Undegoes autoproteolytic activation.
DISEASE: Defects in TMPRSS3 are a cause of childhood-onset autosomal recessive neurosensory deafness 8 (DFNB8) [MIM:601072]
DISEASE: Defects in TMPRSS3 are a cause of congenital autosomal recessive neurosensory deafness 10 (DFNB10) [MIM:605316].
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
SIMILARITY: Contains 1 SRCR domain.
SIMILARITY: Contains 1 LDL-receptor class A domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
               Seems to be capable of activating
                                                                                                                                                                                                          Name=T; Synonyms=Truncated, TADG-12V;
IsoId=P57727-4; Sequence=VSP_005393, VSP_005394;
TISSUE SPECIFICITY: Expressed in many tissues including fetal
cochlea. Isoform T is found at increased levels in some
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zymogen
                                               SUBCELLULAR LOCATION: Type II membrane protein. Endoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Signal-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL)
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MIM, 605316; -..

GO; GO:0016021; C:integral to membrane; NAS.

GO; GO:0006508; P:proteolysis and peptidolysis; NAS.

InterPro; IPR001314; Chymotrypsin.

InterPro; IPR001254; Ser_protease_Try.

InterPro; IPR00190; Srcr_receptor.

Pfam; PF00089; trypsin; 1.

PRART; SM00192; CHYMOTRYPSIN.

SMART; SM00192; LDLa; 1.

SMART; SM00200; Tryp_SPC; 1.

PROSITE; PS00420; SRCR_1; FALSE_NEG.

PROSITE; PS00420; SRCR_2; 1.

PROSITE; PS00420; SRCR_1; FALSE_NEG.

PROSITE; PS00420; SRCR_1; FALSE_NEG.

PROSITE; PS00430; TRYPSIN DOM; 1.

PROSITE; PS00134; TRYPSIN HIS; 1.
                                                                                    Event=Alternative splicing; Named isoforms=4;
Name=A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hydrolase, Serine protease, Transmembrane, Si
Endoplasmic reticulum, Deafness, Alternative
                                                                                                                                             Name=B; Synonyms=C;
IsoId=P57727-2; Sequence=VSP_005391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EXTRACELLULAR
                                                                                                                              IsoId=P57727-1; Sequence=Displayed;
                                                                                                                                                                                              IsoId=P57727-3; Sequence=VSP_
                Probable protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF201380; AAG37012.1; --
EMBL; AB038157; BAB20077.1; --
EMBL; AB038158; BAB20078.1; --
EMBL; AB038159; BAB20079.1; --
EMBL; AB038160; BAB20080.1; --
HSSP; P00763; 1DPO.
MEROPS; S01.079; --
Genew; HGNC:11877; TMPRSS3.
MIM; 605511; --
MIM; 605316; --
MIM; 605316; --
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                                                                               ALTERNATIVE PRODUCTS
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108
              FUNCTION: 1
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LDL-RECEPTOR CLASS A

c c	390 LIGGVDSCQGPDVCQERRLWRLVGAISFGIGCAEVNKFGVITKVISFL	282 A	450 RDL 452		RESULT 6 TMS2 HIMAN	TMS2_HUMAN STANDARD; PRT; 492 AA.	015393; Q9BXX1;		28-FEB-2003 (Rel. 41, Last annotation update)	Transmembrane protease	Homo sapiens (Human).		NCBI_TaxID=9606;	[1] SECHENCE BEOM N A	SECUENCE FROM N.A. MEDLINE=97468144; PubMed=9325052;	Paoloni-Giacob	Anconarakis S.E.; "Cloning of the TMPRSS2 gene, which encodes a novel serine p	with transmembrane, LDLRA, and SRCR domains and maps			MEDLINE=21309069; PubMed=11414763;		"Mutation analyses of 268 candidate genes in human tumor cei			MEDLINE=21139112; PubMed=11245484;	Arar D.E.H., Vlvanco Raitano A.B., Jakobo	"Catalytic cleavage of the androgen-regula	in its secretion by prostate and prostate cand Cancer Res. 61:1686-1692(2001).	[4]	> TISSUE SPECIFICITY.   WRDLINE=21104370: PibMed=11169526:	Vaarala M.H., Porvari K.S., Kellokumpu S., Kyllonen A.P., Vihk	"Expression of transmembrane serine protease TMPRSS2	J. Pathol. 193:134-140(2001).	-1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ACTIVATED	CLEAVAGE AND SECRETED.	EXPRESSED IN PROSTATE, COLON, STOMACH, AND SALIVARY GLAND.	-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI	-:- SIMILARIII: Contains 1 SRCR domain. -:- SIMILARIIY: Contains 1 LDL-receptor class A domain.		This SWISS-PROT entry is copyright. It is pro	between the swips institute of bioinformatics and the the European Bioinformatics Institute. There are no res	use by non-profit institutions as long as	modified and this statement is not removed.	entries requires a license agreement (see nuup://www.isp or send an email to license@isb-sib.ch).		EMBL; U/5329; AAC51/84.1; ~. EMBL: AF123453: AAD37117.1:	AF270487; AAK29280.1	HSSP; P00763; 1DPO. MEROPS; S01.247;	Genew, HGNC:11876; TMPRSS2.	MIM; 602060; GO: GO:0005887: C.integral to plasma membrane. Mas	corocology, criticegrat co prasila memorana,
	<u> </u>	Λ <sub>Ο</sub>	qu		RE RE		AC	I C	TO		SO		; <u>xo</u>	RN 0		RA	RA	RT	H K	RP	RX	RA		RR	- A			RT	RI	RN		RA		RI	8	3.5	) <sub>C</sub>						8	86	 	- B	DR DR	DR	 DR DR	DR	 D. D.R.	-
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R InterPro; IPR001314; Chymotrypsin.
R InterPro; IPR001254; Ser_brotease_Try.
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R InterPro; IPR001254; Ser_brotease_Try.
R InterPro; IPR001190; Srcr_receptor.
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R PROSITE; PS00135; TRYPSIN SER; 1.
R Hydrolase; Serine protease; Transmembrane; Signal-anchor; Zymogen; Polymorphism.
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XR TISSUE=Pancreas, and Spleen;

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XR Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

XR Strausberg R.L., Feingold E.A., Grouse L.H., Schaefer G.E.,

XR Altschul S.F., Zeeberg B., Budgner L., Schaefer G.E., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Marx S.I., Wang J., Hsieh F.,

Altschul S.F., Jordan H., Moore T., Marx S.I., Wang J., Hsieh F.,

A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

XR Stapleton M.J., Usdin T.B., Toshiyuki S., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

XR Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

XR Richards S., Warley D.M., Sodergren B.J., Lu X., Glibs R.A.,

Rahes J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

XR Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Blakesley R.W., Krzywinski M.I., Skalska U., Smailus D.E.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length

Human and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mammalian cell growth.";
Proc. Natl. Acad. Sci. U.S.A. 90:7181-7187(1993).
-!- FUNCTION: Plays an essential role in cell growth and maintenance
of cell morphology.
-!- SUBCELLULAR LOCATION: Type II membrane protein.
-!- TISSUE SPECIFICITY: Present in most tissues, with the highest
level in liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=88209431; PubMed=2835076;
Leytus S.P., Loeb K.R., Hagen F.S., Kurachi K., Davie B.W.;
"A novel trypsin-like serine protease (hepsin) with a putative
transmembrane domain expressed by human liver and hepatoma cells.";
Biochemistry 27:1067-1074(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=93348237; PubMed=8346233;
Torres-Rosado A., O'Shea K.S., Tsuji A., Chou S.H., Kurachi K.;
"Hepsin, a putative cell-surface serine protease, is required for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHARACTERIZATION.
MEDLINE=91358502; PubMed=1885621;
Tsuji A., Torres-Rosado A., Arai T., le Beau M.M., Lemons R.S., Chou S.H., Kurachi K.;
"Hepsin, a cell membrane-associated protease. Characterization, tissue distribution, and gene localization.";
U. Biol. Chem. 266:16948-16953(1991).
                                                                                                                                                                                                                                                           P05981;
01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Serine protease hepsin (EC 3.4.21.-) (Transmembrane protease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI
                                                                                                                                                                                                                                417 AA
                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                STANDARD;
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491
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                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL).

CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
EXTRACELLULAR (POTENTIAL).
SERINE PROTEASE.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SDKLGSFPSLAVAKIIIIEFNPMYP-----KDNDIALMKLQFPLTFSGTVRPICLPF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                               ease; Transmembrane; Signal-anchor.
SERINE PROTEASE HEPSIN, NON-CATALYTIC
CHAIN (POTENTIAL).
SERINE PROTEASE HEPSIN, CATALYTIC CHAIN
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15;
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B2086FF661E551D7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            417;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94; Indels
                                                                                                                                                                                                                                   membrane; TAS.
maintenance; TAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31.6%; Score 505.5; DB 1
41.1%; Pred. No. 8.9e-40;
ive 36; Mismatches 94
                                                                                                          EMBL; M18930; AAA36013.1;

EMBL; X07732; CAA30558.1;

EMBL; X07732; CAA30558.1;

EMBL; X00702; CAA30558.1;

EMBL; BC025716; AAH25716.1;

PIR; S00845; S00845.

HSSP; P00763; 1DPO.

MEROPS; S01.224;

Genew; HGNC:5155; HPN.

MIM; 142440;

GO; GO:0005887; C:integral to plasma memb GO; GO:0008151; P:cell growth and/or main InterPro; IPR001314; Chymotrypsin.

InterPro; IPR001324; Ser_protease_Try.

Pfam; PF00089; trypsin; 1.

PRINTS; PR00722; CHYMOTRYPSIN.

SMART; SM00020; Tryp SPC; 1.

PROSITE; PS00134; TRYPSIN_HIS; 1.

PROSITE; PS00134; TRYPSIN_HIS; 1.

PROSITE; PS00135; TRYPSIN_HIS; 1.

Hydrolase; Serine protease; Transmembrane CHAIN
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103 203

57 257

3 353

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45011 MW;
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Best Local Similarity 41.1
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DOMAIN
ACT SITE
ACT SITE
ACT SITE
DISÜLFID
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CARBOHYD
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=91185335; PubMed=2127931;
Kashiwabara S., Baba T., Takada M., Watanabe K., Yano Y., Arai Y.;
"Primary structure of mouse proacrosin deduced from the cDNA sequence and its gene expression during spermatogenesis.";
J. Biochem. 108:785-791(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chouse proacrosin gene: nucleotide sequence, diploid expression, and chromosomal localization.";
Genomics 11:828-834(1991).

-!- FUNCTION: ACROSIN IS THE MAJOR PROTEASE OF MAMMALIAN SPERMATOZOA.

IT IS A SERINE PROTEASE OF TRYPSIN-LIKE CLEAVAGE SPECIFICITY, IT
IS SYNTHESIZED IN A ZYMOGEN FORM, PROACROSIN AND STORED IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACROSOME.
-!- CATALYTIC ACTIVITY: Hydrolysis of Arg-|-Xaa and Lys-|-Xaa bonds;
preferential cleavage Arg-|-Xaa >> Lys-|-Lys >> Lys-|-Xaa.
-!- SUBUNIT: HEAVY CHAIN (CATALYTIC) AND A LIGHT CHAIN LINKED BY TWO DISULFIDE BONDS.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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MEDLINE=92147126; PubMed=1783391;
Kremling H., Keime S., Wilhelm K., Adham I.M., Hameister H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=92041732; PubMed=1939002;
Watanabe K., Baba T., Kashiwabara S., Okamoto A., Arai Y.
"Structure and organization of the mouse acrosin gene.";
J. Biochem. 109:828-833(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Mouse preproacrosin: cDNA sequence, primary structure postmeiotic expression in spermatogenesis."; Differentiation 42:160-166 (1990).
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                                                                             01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Acrosin precursor (EC 3.4.21.10).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=90255839; PubMed=2111255;
Klemm U., Maier W.-M., Tsaousidou S., Adham
Engel W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOINED.
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                                                       STANDARD;
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HSSP; P00763; 1DPO.
MEROPS; S01.223; -.
                                                   ACRO MOUSE
P23578;
01-NOV-1991
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RESULT 8
ACRO_MOUSE
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STANDARD,
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MGD; MGI:102849; K1kb1
                                                                                                                                                                                                                                     (Mouse)
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                                                                                                                                                                                                                                   Mus musculus
                                                                                                                            KAL MOUSE P26262;
                                 233
                                                                                                   RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q -> RK (IN REF. 3; CAA36704).
QI -> RNT (IN REF. 3; AAA40124).
TCYVTGW -> LLRDWV (IN REF. 3; AAA40124).
YI -> IH (IN REF. 3; AAA40124).
EK -> RE (IN REF. 3; CAA36704/AAA40124).
VDS -> ARQ (IN REF. 3; CAA36704/AAA40124).
YUSAAA0124.
FVVVGITSWGVGCA -> LCGRGDHELGGRLC (IN REF. 3; AAA40124 AND 4).
QP -> PA (IN REF. 3; CAA36704/AAA40124).
L -> F (IN REF. 3; CAA36704/AAA40124).
H -> Y (IN REF. 3; CAA36704/AAA40124).
SQYSGPRNYHYRFSTFEPLSNKPSEPFLHS -> PSTVDKE LPLPLHV (IN REF. 3; CAA36704/AAA40124).
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BY SIMILARITY.

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BY SIMILARITY.

N-LINKED (GLCNAC. . .) (BY SIMILARITY).

CHARGE RELAY SYSTEM (BY SIMILARITY).

CHARGE RELAY SYSTEM (BY SIMILARITY).

CHARGE RELAY SYSTEM (BY SIMILARITY).

CHARGE RELAY SYSTEM (BY SIMILARITY).

MISSING (IN REF. 3; CAA36704/AAA40124).

VUV. -> AG (IN REF. 3; CAA36704/AAA40124).

VV -> AG (IN REF. 3; CAA36704/AAA40124).

T -> A (IN REF. 3; CAA36704/AAA40124).

C -> F (IN REF. 3; CAA36704/AAA40124).

QL -> HV (IN REF. 3; CAA36704/AAA40124).

QL -> HV (IN REF. 3; CAA36704/AAA40124).

QL -> HV (IN REF. 3; CAA36704/AAA40124).

QL -> HV (IN REF. 3; CAA36704/AAA40124).

QL -> HV (IN REF. 3; CAA36704/AAA40124).

QL -> HV (IN REF. 3; CAA36704/AAA40124).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QQERYVQKIVIHEKYNVYTEGNDIALLKITPPVTCGNFIGPCCLPHF-KAGPPQIPHTCY
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                                                                                                               ease; Glycoprotein; Zymogen; Sperm; Signal
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O -> RK (IN REF. 3; AAA4012
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BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4CC6EAD56CB51F54 CRC64;
                                                                                                                                                      ACROSIN LIGHT CHAIN
ACROSIN HEAVY CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 499; DB 1;
Pred. No. 3.8e-39;
                                                                                                                                                                                             SERINE PROTEASE
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001314; Ser_protease_Tr
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SWART; SM00020; Tryp_SPc; 1.
PROSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00135; TRYPSIN DOM; 1.
PROSITE; PS00135; TRYPSIN DOM; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
Hydrolase; Serine protease; GlycoprosiGNAL 20 42 ACROSIN CHAIN 20 436 ACROSIN PROPEP 20 42 ACROSIN PROPEP 25 155 INTERCH DISULFID 25 163 INTERCH DISULFID 25 163 INTERCH DISULFID 210 226 BY SIMI DISULFID 237 267 BY SIMI DISULFID 237 267 BY SIMI DISULFID 237 267 BY SIMI DISULFID 211 211 N-LINKE CARBOHYD 211 211 N-LINKE ACT_SITE 89 BY SIMI CARBOHYD 211 211 CHARGE ACT_SITE 241 241 CHARGE CONFLICT 10 144 VLVUA -
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Matches 112; Conser
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

STRAIN=BALB/c; TISSUB=Liver;

MEDLINE=91090844; PubMed=2264928;

Seidah N.G., Sawyer N., Hamelin J., Mion P., Beaubien G.,

Brachpapa L., Rochemont J., Mbikay M., Chretien M.;

Brachpapa L., Rochemont J., Mbikay M., Chretien M.;

Brachpapa L., Rochemont J., Mbikay M., Chretien M.;

Mouse plasma kallikrein: cDNA structure, enzyme characterization,

The mode plasma kallikrein and mRNA levels among species.";

DNA Cell Biol. 9:737-748(1990).

-!- FUNCTION: THE ENZYME CLEAVES LYS-ARG AND ARG-SER BONDS. IT

ACTIVATES, IN A RECIPROCAL REACTION, FACTOR XII AFTER ITS BINDING

TO A NEGATIVELY CHARGED SURFACE. IT ALSO RELEASES BRADYKININ FROM

HWM KININOGEN AND MAY ALSO PLAY A ROLE IN THE RENIN-ANGIOTENSIN

SYSTEM BY CONVERTING PRORENIN INTO RENIN.

-!- CATALYTIC ACTIVITY: Cleaves selectively Arg-|-Xaa and Lys-|-Xaa

bonds, including Lys-|-Arg and Arg-|-Ser bonds in (human)

kininogen to release bradykinin.

C -!- SUBUNIT: THE ZYMOGEN IS ACTIVATED BY FACTOR XIIA, WHICH CLEAVES

THE MOLECULE INTO A LIGHT CHAIN, WHICH CONTAINS THE ACTIVE SITE,

AND A HEAVY CHAIN, WHICH ASSOCIATES WITH HWW KININOGEN. THESE

C -!- SUBUNITY: BELONGS TO PEPTIDASE FAMILY SI. PLASMA KALLIKREIN

STHERANTLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BINDING
NIN FROM
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Plasma kallikrein precursor (EC 3.4.21.34) (Plasma prekallikrein)
(Kininogenin) (Fletcher factor).
                                                                                                                                                                    240 DSGGPLMCRDNVDSPFVVVGITSWGVGCARAKRPGVYTATWDYLDWI
                                                                                                                           DSGGPLMYQSD---QWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWI
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InterPro; IRR0001314; Chymotrypsin.
InterPro; IRR003014; PAN.
InterPro; IRR01254; Ser_protease_Tr
Pfam; PF00024; PAN; 4.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00005; APPLEDOMAIN.
PRINTS; PR00722; CHYMOTRYPSIN.
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SMART; SM00020; Tryp SPC; 1.
PROSITE; PS00495; APPLE; 4.
PROSITE; PS50240; TRYPSIN DOM;
PROSITE; PS00134; TRYPSIN HIS;
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PIR; A36557; KQMSPL.
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                                     Glycoprotein; Plasma; Zymogen; Si
tion; Inflammatory response; Liver
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                                                                                                                                         PLASMA KALLIKREIN HEAVY CI
PLASMA KALLIKREIN LIGHT CI
APPLE 1.
APPLE 2.
APPLE 3.
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SERINE PROTEASE.
N-LINKED (GLCNAC. ..)
N-TINKED (GLCNAC. ..)
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(PROBABLE) .
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CHARGE RELAY SYSTEM.
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43.5%; Pred. No. 2.7e-38;
ive 41; Mismatches 77
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Last annotation update)
(EC 3.4.21.-).
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PROSITE; PS00135; TRYPSIN SER; 1.

Hydrolase; Serine protease; Glycopreseat.

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Best Local Similarity 43.5%;
Matches 103; Conservative 4
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EPS MOUSE

D HEPS MOUSE STANDARD;

C 035453; Q9CW97;

T 15-JUL-1998 (Rel. 36, Cref. 15-SEP-2003 (Rel. 42, Last. 15-SEP-2003 (Rel. 42, Last. 15-SEP-2003 (Rel. 42, Last. 15-SEP-2003 (Rel. 42, Last. 15-SEP-2003 (Rel. 42, Last. 15-SEP-2003 (Rel. 42, Last. 15-SEP-2003 (Rel. 42, Last. 15-SEP-2003 (Rel. 42, Last. 15-SEP-2003 (Rel. 42, Last. 15-SEP-2003 (Rel. 42, Last. 15-SEP-2003 (Rel. 42, Last. 15-SEP-2003 (Rel. 42, Last. 15-SEP-2003 (Rel. 42, Last. 15-SEP-2003 (Rel. 42, Last. 15-SEP-2003 (Rel. 42, Last. 15-SEP-2003 (Rel. 42, Last. 15-SEP-2003 (Rel. 42, Last. 15-SEP-2003 (Rel. 42, Last. 15-SEP-2003 (Rel. 42, Last. 15-SEP-2003 (Rel. 42, Last. 15-SEP-2003 (Rel. 42, Last. 15-SEP-2003 (Rel. 42, Last. 15-SEP-2003 (Rel. 42, Last. 15-SEP-2003 (Rel. 42, Last. 15-SEP-2003 (Rel. 42, Last. 15-SEP-2003 (Rel. 42, Last. 15-SEP-2003 (Rel. 42, Last. 15-SEP-2003 (Rel. 42, Last. 15-SEP-2003 (Rel. 42, Last. 15-SEP-2003 (Rel. 42, Last. 15-SEP-2003 (Rel. 42, Last. 15-SEP-2003 (Rel. 42, Last. 15-SEP-2003 (Rel. 42, Last. 15-SEP-2003 (Rel. 42, Last. 15-SEP-2003 (Rel. 42, Last. 15-SEP-2003 (Rel. 42, Last. 15-SEP-2003 (Rel. 42, Last. 15-SEP-2003 (Rel. 42, Last. 15-SEP-2003 (Rel. 42, Last. 15-SEP-2003 (Rel. 42, Last. 15-SEP-2003 (Rel. 42, Last. 15-SEP-2003 (Rel. 42, Last. 15-SEP-2003 (Rel. 42, Last. 15-SEP-2003 (Rel. 42, Last. 15-SEP-2003 (Rel. 42, Last. 15-SEP-2003 (Rel. 42, Last. 15-SEP-2003 (Rel. 42, Last. 15-SEP-2003 (Rel. 42, Last. 15-SEP-2003 (Rel. 42, Last. 15-SEP-2003 (Rel. 42, Last. 15-SEP-2003 (Rel. 42, Last. 15-SEP-2003 (Rel. 42, Last. 15-SEP-2003 (Rel. 42, Last. 15-SEP-2003 (Rel. 42, Last. 15-SEP-2003 (Rel. 42, Last. 15-SEP-2003 (Rel. 42, Last. 15-SEP-2003 (Rel. 42, Last. 15-SEP-2003 (Rel. 42, Last. 15-SEP-2003 (Rel. 42, Last. 15-SEP-2003 (Rel. 42, Last. 15-SEP-2003 (Rel. 42, Last. 15-SEP-2003 (Rel. 42, Last. 15-SEP-2003 (Rel. 42, Last. 15-SEP-2003 (Rel. 42, Last. 15-SEP-2003 (Rel. 42, Last. 15-SEP-2003 (Rel. 42, Last. 15-SEP-2003 (Rel. 42, Last. 15-SEP-2003 (Rel. 42, Last. 15-SEP-2003 (Rel. 42, Last. 15-SEP-2003 (Rel. 42
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Craniata, Vertebrata, Euteleostomi, Sciurognathi, Muridae, Murinae, Mus

hordata; (

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOPORM 1).

SEQUENCE FROM N.A. (ISOPORM 1).

STRAIN=C57BL/6J; TISSUE=Kidney;

Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Ratawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

Alzawa M., Nishi K., Kiyosawa H., Kando S., Yamanaka I.,

Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kasukawa T., Saito R.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Ruehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Ruehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Ruehl F., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Ruehl P., Lewis S., Matsuo Y., Ridaido H., Baldarelli R., Barsh G.,

Schriml L.M., Staubli F., Suzuki R., Tomita M., Gariboldi M.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Ryordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Ryordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Ryunshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Hayashizaki Y.,

Ryunctional annotation of a full-length mouse cDNA collection.";

Ryunchon Plant Rodrial Foll From Resolution of a full-length mouse cDNA collection.";
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                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
MEDLINE=9933944; PubMed=10411637;
Kawamura S., Kurachi S., Deyashiki Y., Kurachi K.;
"Complete nucleotide sequence, origin of isoform and functional characterization of the mouse hepsin gene.";
Eur. J. Blochem. 262:755-764(1999).
                                                                                                                                                                               E.W.;
serine
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SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CAUTION: Ref.3 sequence differs from that shown due to
frameshifts in positions 155, 191 and 233.
                                                                                                        TISSUE=Liver;
MEDLINE=98058912; PubMed=9395459;
Vu T.-K.H., Liu R.W., Haaksma C., Tomasek J.J., Howard E "Identification and cloning of the membrane-associated sprotease, hepsin, from mouse preimplantation embryos."; J. Biol. Chem. 272:31315-31320(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of cell morphology.
SUBCELLULAR LOCATION: Type II membrane protein.
ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
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IsoId=035453-2; Sequence=VSP_007232;
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Note=Minor isoform;
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EMBL; AK002694; BAB22289.2; ALT_FRAME.
HSSP, P00763; 1DPO.
MEROPS; S01.224; -.
MGD; MGI:1196620; Hpn.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR001190; Srcr_receptor.
                                                                            FROM N.A. (ISOFORM 2).
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NCBI_TaxID=10090;
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PRINTS; PR00722;
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Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                       (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                            CATALYTIC CHAIN
                                                                                                                              SIGNAL-ANCHOR (IIFE-II MEMBRANE FROIDER
(POTENTIAL).
SETRACELLULAR (POTENTIAL).
SERINE PROTEASE.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
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BY SIMILARITY.
BY SIMILARITY.
CHARGE (GLCNAC. . .) (POTENTIAL).
MISSING (in isoform 2).
//FTIG=VSP (07232.
L -> F (IN REF. 3).
G -> R (IN REF. 3).
C -> R (IN REF. 3).
NR -> ET (IN REF. 3).
R -> L (IN REF. 3).
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                                                                       SERINE PROTEASE HEPSIN, NON-CATALYTIC
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                                                                                                                                                                                                                                                                                                                                             30.7%; Score 491.5; DB 1; Length 436; llarity 40.2%; Pred. No. 1.9e-38; Conservative 39; Mismatches 93; Indels 15
SMART; SM00202; SR; 1.

SMART; SM00020; Tryp SPc; 1.

PROSITE; PS50240; TRYPSIN DOM; 1.

PROSITE; PS00134; TRYPSIN HIS; 1.

PROSITE; PS00135; TRYPSIN SER; 1.

Hydrolase; Serine protease; Transmembrane; Signal-anchor; Alternative splicing.

CHAIN

CHAIN

SERINE PROTEASE HEPSIN, NON-
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                                                                                 CHAIN (POTENTIAL).
SERINE PROTEASE HEPSIN,
(POTENTIAL).
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Last annotation update)
3.4.21.10).
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Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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CROOSIN ACR.
S Rattus norvegicus (Rat)
S Rattus norvegicus (Rat)
C Bukaryota; Metazoa; Chon
C Mammalia; Eutheria; Rode
K NCBI_TaxID=10116;
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SERINE PROTEASE.
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STRAIN=Sprague-Dawley; TISSUE=Testis;
MEDLINE=92031708; PubMed=1932123;
Klemm U., Flake A., Engel W.;
"Rat sperm acrosin: cDNA sequence, derived primary structure and phylogenetic origin.";
Biochim. Biophys. Acta 1090:270-272(1991).
Biochim. Biophys. Acta 1090:270-272(1991).
IT IS A SERINE PROTEASE OF TRYPSIN-LIKE CLEAVAGE SPECIFICITY, IT IS A SERINE PROTEASE OF TRYPSIN-LIKE CLEAVAGE SPECIFICITY, IT IS A SERINE PROTEASE OF TRYPSIN-LIKE CLEAVAGE SPECIFICITY, IT IS SYNTHESIZED IN A ZYMOGEN FORM, PROACROSIN AND STORED IN THE
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preferential cleavage Arg-|-Xaa >> Lys-|-Lys >> Lys-|-Xaa.
-!- SUBUNIT: HEAVY CHAIN (CATALYTIC) AND A LIGHT CHAIN LINKED BY TWO DISULFIDE BONDS.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
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RISSP; S18407; S18407.

RISSP; PO0763; 1DPO.

RISSP; PO0763; 1DPO.

RISSP; PO0763; 1DPO.

RISSP; PO0763; 1DPO.

RICEPPO; IPR001254; Ser_protease_Try.

PRMINTS; PR00722; CHYMOTRYPSIN.

RMART; SM0020; Tryp. SPC; 1.

PROSITE; PS00134; TRYPSIN DOM; 1.

PROSITE; PS00134; TRYPSIN HIS; 1.

PROSITE; PS00135; TRYPSIN SER; 1.

RYDROIDS Serine protease; Glycoprotein; Zymogen; Sperical Name of All Strain Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Serine Seri
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22 N-
211 N-
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REMBL; M30282; AAA41463.1; -.
REMBL; M58590; AAA42069.1; -.
REMBL; M58590; AAA42069.1; -.
RESP; P00750; 1RTF.
RENOPS; S01.212; -.
RENOPS; S01.212; -.
RENOPS; S01.212; -.
RENOPS; S01.212; -.
RETECTO; 1PR0001314; Chymotrypsin.
RICETORO; 1PR0001314; PAN.
RICETORO; 1PR0001314; PAN.
RICETORO; 1PR0001314; PAN.
REMINES; PR000024; PAN.
REMINES; PR00005; APPLEDOMAIN.
REMINES; PR000020; Tryp. SPC: 1.
REMINES; PR00132; APPLE; 4.
REMINES; PR00134; TRYPSIN. DOM; 1.
REMOSITE; PS00134; TRYPSIN DOM; 1.
REMOSITE; PS00134; TRYPSIN DOM; 1.
REMOSITE; PS00135; TRYPSIN ERF; 1.
REMOSITE; PS00135; TRYPSIN ERF; 1.
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42.2%; Pred. No. 5.2e-38;
cive 45; Mismatches 76
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638 AA;
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N [2]

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SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

X MEDLINE=90091743; PubMed=2598771;

A Seidah N.G., Ladenheim R., Mbikay M., Hamelin J., Lutfalla G.,

A ROUGEON F., Lazure C., Chretien M.;

ROUGEON F., Lazure C., Chretien M.;

DNA 8:563-574(1989).

C -!- FUNCTION: THE BNZYME CLEAVES LYS-ARG AND ARG-SER BONDS. IT

ACTIVATES, IN A RECIPROCAL REACTION, FACTOR XII AFTER ITS BINDING

C ACTIVATES, IN A RECIPROCAL REACTION, FACTOR XII AFTER ITS BINDING

C ACTIVATES, IN A RECIPROCAL REACTION, FACTOR XII AFTER ITS BINDING

C ACTIVATES AND MAY ALSO PLAY A ROLE IN THE RENIN-ANGIOTENSIN

SYSTEM BY CONVERTING PRORENIN INTO RELIN.

C CATALYTIC ACTIVITY: Cleaves selectively Arg-|-xaa and Lys-|-xaa

C CATALYTIC ACTIVITY: Cleaves selectively Arg-|-xaa

C CATALYTIC ACTIVITY: Cleaves bradykinin.

C CATALYTIC ACTIVITY: THE ZYNGGEN IS ACTIVATED BY FACTOR XIIA, WHICH CLEAVES

C CATALYTIC BLONGEN IS ACTIVATED BY FACTOR XIIA, WHICH CLEAVES

C CHAINS ARE LINKED BY ONE OR MORE DISULFIDE BONDS.

C CALAINS ARE LINKED BY ONE OR MORE DISULFIDE BONDS.

C CALAINS ARE LINKED BY ONE OR MORE DISULFIDE BONDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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       232
                      IIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPEGGVDTCQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=1993180;
nski-Chupin I., Mattei M.-G., Mbikay M., Chretien M.
                                                                                                                                                                                                                                                                                                                                                                 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus
NCBI TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            romosomal localization of plasma kallikrein.";
                                                                                                                                                                                               KAL RAT STANDARD; PRT; 638 AA.
P14272;
01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Plasma kallikrein precursor (EC 3.4.21.34) (Plasma prekallikrein)
(Kininogenin) (Fletcher factor).
                                                                              276
                                                                           --WHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWI
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M62346; AAA74563.1
M62347; AAA74563.1
M62349; AAA74563.1
M62350; AAA74563.1
M62351; AAA74563.1
M62352; AAA74563.1
M62353; AAA74563.1
M62354; AAA74563.1
M62354; AAA74563.1
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Beaubien G., Rosinski-(
Seidah N.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Gene structure and ch
Biochemistry 30:1628-1
                                                                        DSGGPLMYQSDQ-
                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat
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EMBL; M62346; A
EMBL; M62347; A
EMBL; M62349; A
EMBL; M62350; A
EMBL; M62351; A
EMBL; M62352; A
EMBL; M62352; A
EMBL; M62353; A
EMBL; M62353; A
EMBL; M62353; A
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    173
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(PROBABLE). (PROBABLE). (PROBABLE). (PROBABLE).

CHAIN.

HEAVY LIGHT

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Gaps

16;

38; 76; Indels

Length 638;

161

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                                                                                                                                                                                                                                                                                                                              from
                                                                                                                                                                                                                                                             PSEQUENCE FROM N.A.

SEQUENCE FROM N.A.

TISSUE=Brain;

PubMed=11741986;

Yamaguchi N., Okui A., Yamada T., Nakazato H., Mitsui S.;

Laspinesin/TMPRSS5, a novel transmembrane serine protease, cloned from thuman spinal cord.";

J. Biol. Chem. 277:6806-6812(2002).

-!- SUBCELLULAR LOCATION: Type II membrane protein (Potential).

-!- SUBCELLULAR LOCATION: Type II membrane protein (Potential).

-!- SUBCELLULAR LOCATION: Type II membrane protein (Potential).

-!- SUBCELLULAR LOCATION: Type II membrane protein (Potential).

-!- SUBCELLULAR LOCATION: Type II membrane protein (Potential).

-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
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Catarrhini; Hominidae; Homo.
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SIMILARITY).
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SIGNAL-ANCHOR (TYPE-II MEMBRANE
                                                                                                                        16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Transmembrane protease, serine 5 (BC 3.4.21.-) (Spinesin)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transmembrane; Signal-anchor;
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EXTRACELLULAR (POTENTIAL)
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CHARGE RELAY SYSTEM (1)
CHARGE RELAY SYSTEM (1)
CHARGE RELAY SYSTEM (1)
CLEAVAGE (POTENTIAL).
BY SIMILARITY.
BY SIMILARITY.
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MIM, 606751; -. IMPROSS5.

MIM, 506751; -. IMPROSS5.

InterPro; IPR001314; Chymotrypsin. InterPro; IPR001254; Ser_protease_Try. InterPro; IPR001254; Ser_protease_Try. InterPro; IPR001254; Ser_protease_Try. InterPro; IPR001254; Ser_protease_Try. PR00178; PR00722; CHYMOTRYPSIN.

SMART; SM00020; Tryp_SPc; 1. PROSITE; PS00134; TRYPSIN DOM; 1. PROSITE; PS00134; TRYPSIN HIS; 1. PROSITE; PS00135; TRYPSIN SER; 1. PROSITE; PS00420; SRCR_1; FALSE_NEG. PROSITE; PS0287; SRCR_2; FALSE_NEG. Hydrolase; Serine protease; Transmembr Glyconrofein
                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                  STANDARD;
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70
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Glycoprotein.
DOMAIN
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Q9H3S3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=129/Sv;
MEDLINE=21153229; PubMed=11231276;
Scarman A.L., Hooper J.D., Boucaut K.J., Sit M.-L., Webb G.C.,
Normyle J.F., Antalis T.M.;
"Organization and chromosomal localization of the murine Testisin gene
encoding a serine protease temporally expressed during
                                                                                                                                                                                                                                                                                                                                                                                                       278
                                                                                                                                                                                                           KIVGGYALDVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHCFR--KHTDVFNWKVRAG
                                                                                                                                                                                                                            SDKLGSFPSLAVAKIIIIEF---NPMYPKDN---DIALMKLOFPLTFSGTVRPICLPFFD
                                                                                                                                                                                                                                                                                     277 ---LVSHSAVRPHQGALVERIIPHPLYSAQNHDYDVALLRLQTALNFSDTVGAVCLPAKE
                                                                                                                                                                                                                                                                                                                           163 BELTPATPLWIIGWGFTKONGGKMSDILLOASVQVIDSTRCNADDAYQGEVTEKMMCAGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wong G.W., Li L., Madhusudhan M.S., Krilis S.A., Gurish M.F.,
Rothenberg M.E., Sali A., Stevens R.L.;
"Tryptase 4, a new member of the chromosome 17 family of mouse serine
proteases.";
                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                       223 PEGGVDTCQGDSGGPLMY-QSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 3-321 FACT.
STRAIN=CS7BL/6J; TISSUE=Testis;
MEDLINE=21085660; PubMed=11217851;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y. Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S. Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I. Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R. Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
                                                            (POTENTIAL) .
                                                                                          . .) (POTENTIAL) . .) (POTENTIAL)
                                                 (POTENTIAL)
                                                                                                                                                                                  12;
                                                                                                                                                      Length 457;
                                                                                                                                                                                Indels
                                                                                                                        CRC64;
                                                                                                                                                 th 30.4%; Score 487; DB 1; L Similarity 39.7%; Pred. No. 5.4e-38; 94; Conservative 44; Mismatches 87;
BY SIMILARITY.
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Eur. J. Biochem. 268:1250-1258(2001).
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  259
390
429
163
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84
8574 MW;
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STRAIN=BALB/c; TISSUE=Testis;
PubMed=11259427;
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  243
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457 AA;
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Best Local
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TEST MOUSE
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Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., A Sakai K., Okido T., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., A Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., A Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., A Suzuki H., Toyo-oka K., Wang K.H., Weiz C., Whittaker C., Wilming L., Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hayashizaki Y., Runctional annotation of a full-length mouse cDNA collection."; L. FUNCTION: COULD REGULATE PROTEOLYTIC EVENTS ASSOCIATED WITH C. TESTICULAR GERM CELL MATURATION.

C. I. FUNCTION: Attached to the membrane by a GPI-anchor (Potential).

C. I. SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (Potential).

C. I. ENSUE SPRCIFICITY: Testis.

C. I. DEVELOPMENTAL STAGE: EXPRESSED IN POST-MEIOTIC TESTICULAR GERM CELLS.

C. I. SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.

C. I. CAUTION: REF: SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A STOP CODON IN POSITION 315.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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REMEL; A7005145; AAK29360.1; -

REMEL; A7005145; AAK29360.1; -

REMEL; A7206710; AAK644407.2; -

REMEL; A7206710; AAK644407.2; -

REMEL; A7206711; -: NOT_ANNOTATED_CDS.

REMEL; A720671; -: NOT_ANNOTATED_CDS.

REMEL; A720671; -: NOT_ANNOTATED_CDS.

REMEL; A720671; -: NOT_ANNOTATED_CDS.

REMEL; A720671; -: NOT_ANNOTATED_CDS.

REMEL; A720671; -: NOT_ANNOTATED_CDS.

REMEL; A720671; -: NOT_ANNOTATED_CDS.

REMEL; A720671; -: NOT_ANNOTATED_CDS.

REMEL; A720672; CTYPOSIN; 1.

REMEL; REMOUSD; TYPESIN; DOM; 1.

REMEL; REMOUSD; TYPESIN; 1.

REMOUSD; TYPESIN; 1.

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Length 324;

Score 483; DB 1; Pred. No. 8.4e-38;

30.2%;

Similarity

Query Match Best Local (

Match

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                                                                           59
                                                                      GARGKTLVPLLVVVATAAM--ALQSTYLQVDPEKPELQEPDLLSGPCGHRTIPSRIVGGD
                                                                                                                                BNRTDCWVTGWGAIGEDESLPSPNTLQEVQVAIINNSMCNHMYKKPDFRTNIWGDMVCAG
                                                                                                           57 ALDVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHCFRKHTDVFNWKVRAGSDKLGSFP
                                                                                                                                                                                                                                                          166 TPATPLWIIGWGFTKQNGGKMS-DILLQASVQVIDSTRCN---ADDAYQGEVTEKMMCAG
                                       ---VDAAALAAPFDD---DDKIVGGY
                                                                                                                                                                                                               SLWNLQAYSNRYQIEDIFLSPKYSEQYP--NDIALLKLSSPVTYNNFIQPICLLNSTYKF
                                                                                                                                                                                      SL----AVAKIIIIE-----FNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFDEEL
                                                                                                                                                                                                                                                                                                                                           276
  Gaps
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"Organization and alternative splicing of CACNAIH.";
"Organization and alternative splicing of CACNAIH.";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: MEMBRANE-ANCHORED (Potential).
-!- TISSUE SPECIFICITY: Expressed in many tissues.
-!- POLYMORPHISM: There are two alleles; gamma-I and gamma-II which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and
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-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. TRYPTASE SUBFAMILY
                                                                                                                                                                                                                                                                                                                                     222 IPEGGVDTCQGDSGGPLMYQSDQ-WHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWI
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (VARIANTS GAMMA-1 AND GAMMA-2).
MEDLINE=20302813; PubMed=10843716;
Caughey G.H., Raymond W.W., Blount J.L., Hau L.W., Pallaoro M.,
Wolters P.J., Verghese G.M.;
"Characterization of human gamma-tryptases, novel members of the
chromosome 16p mast cell tryptase and prostasin gene families.";
J. Immunol. 164:6566-6575(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRYG HUMAN STANDARD; PRT; 321 AA.
09NRR2; 09C015; 09NRQ8; 09UBB2;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Tryptase gamma precursor (EC 3.4.21.-) (Transmembrane tryptase)
TPSG1 OR TMT.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=99452974; PubMed=10521469;

WeDLINE=99452974; PubMed=10521469;

Wong G.W., Tang Y., Feyfant E., Sali A., Li L., Li Y., Huang C.,

Friend D.S., Krilis S.A., Stevens R.L.;

"Identification of a new member of the tryptase family of mouse

human mast cell proteases which possesses a novel COOH-terminal
    30;
    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae;
 105;
  Mismatches
                                    GSSOKSRLLLLLVVSNLLLCQGVVSDYKDDDD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biol. Chem. 274:30784-30793(1999)
50;
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111;
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TRYPTASE GAMMA HEAVY CHAIN.

POTENTIAL.

CHARGE RELAY SYSTEM (BY SIMILARITY).

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CHARGE RELAY SYSTEM (BY SIMILARITY).

INTERCHAIN (POTENTIAL).

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A -> V (IN GAMMA-II).

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I -> I (IN GAMMA-II).

FTIG=VAR 012099.

L -> I (IN GAMMA-II).

FTIG=VAR 012099.

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FTIG=VAR 012100.

L -> F (IN GAMMA-II).

FTIG=VAR 012101.

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W -> S (IN REF. 1).
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EMBL; AF195508; AAF76458.1; -.

EMBL; AF175759; AAF03697.1; -.

EMBL; AF27552; AAF03695.1; -.

EMBL; AF27552; AAF03695.1; -.

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EMBL; AF27552; AAF03695.1; -.

EMBL; AF27610.28; -.

EMBL; AF00763; 1DPC.

EMBL; AF00763; 1DPC.

EMBL; AF007624; Ser_protease_Try.

EMBL; AF00089; Lrypsin, 1.

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	Description	O96e86 homo sapien	OBVCA5 MUSCULU	Ogbvel homo sapien	OSCIEC MIS MISCHILL	Ogbve2 homo sanien	090274 rattus norv	Ostroe mis micros	Oskito mis miscuiu	Oscila rattis	OSCITO TATTUS NOTE	Ogdaro xenomia lae	Osubia metting nomi		OBidirl musculus		-
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6	Query Match	79.1	65.5	33.3	33.0	33.0	32.9	32.8	32.7	32.6	32.6	32.6	32.6	32.4	31:8	31.8	31.6
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492.5	87	486	483	481.5	480.5	478.5	478.5	477.5	477.5	477.5	477.5	473.5	470	469.5	468	467	464.5	463	459.5	S	45	•	455	454.5	454		S	452.5
17	8	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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SVVGGVEAPVDSWPWQVSIQXNKQHVCGGSILDPHWILTAAHCFRKYLDVSSWKVRAGSN
                                                                            KLGSFPSLAVAKIIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFDEELTPATP
                                                                                                          ILGNSPSLPVAKIFIAEPNPLYPKEKDIALVKLOMPLTFSGSVRPICLPFSDEVLVPATP
                                                                                                                                                                                               109 SDKLGSFPSLA-VAKIIIIEFNPMY---PKDNDIALMKLQFPLTFSGTVRPICLPFFDEE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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InterPro; 1PR001314; Chymotrypsin.

InterPro; 1PR001254; Ser_protease_Try.
InterPro; 1PR001254; Ser_protease_Try.
InterPro; 1PR001190; Srcr_receptor.

Pfam; PF00089; trypsin; 1.

Pfam; PF00089; trypsin; 1.

RMART; SM00192; LDLa; 1.

SMART; SM00020; SR; 1.

SMART; SM00020; Tryp_SPc; 1.

SMART; SM00020; Tryp_SPc; 1.

PROSITE; PS50287; SRCR 2; 1.

PROSITE; PS00134; TRYPSIN HIS; 1.

PROSITE; PS00135; TRYPSIN HIS; 1.

PROSITE; PS00135; TRYPSIN HIS; 1.

RYdrolase; Protease; Serine protease.

SEQUENCE 537 AA; 58102 MW; A39FF4E8816DAECF CRC64;
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Last annotation update)
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MEDLINE=21167393; PubMed=11267681;
Kim D.R., Sharmin S., Incue M., Kido H.;
"Cloning and expression of novel mosaic serine without a transmembrane domain from human lung."
Biochim. Biophys. Acta 1518:204-209(2001).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
EMBL; AB048797; BAB39742.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33.3%; Score 533; DB 4; 44.0%; Pred. No. 1.4e-44;
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Mosaic serine protease.
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                                                                                                                                                                                                                                                                          GKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPEGGVDTC
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MEDLINE=2144321; PubMed=12149280;

MEDLINE=2144321; PubMed=12149280;

Vuagniaux G., Vallet V., Jaeger N.F., Hummler E., Rossier B.C.;

T "Synergistic Activation of BNaC by Three Membrane-bound Channel-activating Serine Proteases (mCAPI, mCAP2, and mCAP3) and Serum-and alucocorticoid-requiated Kinse (Sgk1) in Xenopus Oocytes.";

J. Gen. Physiol. 120:191-201(2002).

EMBL; ACO21368; AAH21368.1; -.

REBL; ACO21368; AAH21368.1; -.

REBL; ACO3240; ARK85307.1; -.

REBL; ACO324; -.

REBL; ACO3254; ARK85307.1; -.

REPL; ACO3254; ARK85307.1; -.

REPL; ACO3254; ARK85307.1; -.

REPL; ACO3254; ARK85307.1; -.

REPL; ACO3254; ARK85307.1; -.

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REPL; ACO3254; ARK85307.1; -.

REPL; ACO3254; ARK85307.1; -.

REPL; ACO3255; ARK95307.1; -.

REPL; ACO3256; ARK95307.1; -.

REPL; ACO3256; ARK95307.1; -.

REPL; ACO3355; ARK95307.1; -.

REPL; ACO3369; ARK95307.1; -.

REPL; ACO3369; ARK95307.1; -.

REPL; ACO3369; ARK95307.1; -.

REPL; ACO3369; ARK95307.1; -.

REPL; ACO3369; ARK95307.1; -.

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REPL; ACO3369; ARK95307.1; -.

REPL; ACO3369; ARK95307.1; -.

REPL; ACO3369; ARK95307.1; -.

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REPL; ACO3369; ARK95307.1; -.

REPL; ACO3369; ARK95307.1; -.

REPL; ACO3369; ARK95307.1; -.

REPL; ACO3369; ARK95307.1; -.

REPL; ACO3369; ARK95307.1; -.

REPL; ACO3369; ARK95307.1; -.

REPL; ACO3369; ARK95307.1; -.

REPL; ACO336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Buteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                           DQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNMIYNVWKAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel. 20, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
transmembrane protease, serine 4 (Channel-activating
                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65.5%; Score 1048; DB 11; Length 78.6%; Pred. No. 2.9e-96; ive 27; Mismatches 23; Indels
          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                o the EMBL/GenBank/DDBJ databases
        5; DB 4;
4e-118;
                                                  2; Mismatches
     Score 1266;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
     79.1%;
Query Match
Best Local Similarity 97.4
Matches 228; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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RVVGGEEASVDS
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TISSUE=Breast tumor;
Strausberg R.;
Submitted (JAN-2002)
                                                                                            KIVGGYALDVDS
                                                                                                                                                                                 KLGSFPSLAVAK
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Best Local Similarity
Matches 184; Conser
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Q8VCA5,
01-MAR-2002 (
01-MAR-2002 (
01-MAR-2003 (
Similar to tra
protease 2).
                                                                                                                                    172
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225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         349 NETCWITGEGXIKETDEKTSPFLREVQVNLIDFKKCNDYLVYDSYLTPRMMCAGDLRGGR 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DICOGDSGGPLM-YQSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               109 SDKLGSFPSLAVAKIIIIEFNPMYPKDN-DIALMKLQFPLTFSGTVRPICLPFFDEELTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         289 TSNLHQLPEAASISQIIINGNYTDEQDDYDIALIRLSKPLTLSAHIHPACLPMHGQTFGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vertebrata; Euteleostomi;
thi; Muridae; Murinae; Mus
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MEDLINE=21167393; PubMed=11267681;
Kim D.R., Sharmin S., Incue M., Kido H.;
"Cloning and expression of novel mosaic serine proteases with and without a transmembrane domain from human lung.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Buteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33.0%; Score 528; DB 11; Length 471; 43.7%; Pred. No. 3.8e-44; tive 36; Mismatches 94; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=C57BL/6J; TISSUE=Breast tumor;
Strausberg R.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC042878; AAH42878.1; -.
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52535 MW; ED58CFE6B7C3BCC4 CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to mosaic serine protease (Fragment).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae
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protease.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    el. 17, el. 17, el. 23, lel. 23, lel. serine l
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Best Local Similarity 43.7
Matches 104; Conservative
                                                                                                                                                                                                                                                                       PRELIMINARY;
         GGVDTCQGDSGGE
                                     472 GGRDSCQGDSGGP
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01-JUN-2001 (TrEMBLrel
01-MAR-2003 (TrEMBLrel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       471 AA;
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                                                                                                      284 L 284
                                                                                                                                       532 V E
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NON_TER
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109 SDKLGSFPSLA-VAKIIIIEFNPMY---PKDNDIALMKLQFPLTFSGTVRPICLPFFDEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             380 TSNLHQLPEAASIAEIII---NSNYTDEEDDYDIALMRLSKPLTLSAHIHPACLPMHGQT
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGVDTCQGDSGGPLM-YQSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYN 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21332587; PubMed=11439186; Bicknell A.B., Lomthaisong K., Woods R.J., Hutchinson E.G., Bennett H.P.J., Gladwell R.T., Lowry P.J.; "Characterization of a Serine Protease that Cleaves Pro-gamma-Melanotropin at the Adrenal to Stimulate Growth."; Cell 105:903-912 (2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Length 581;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      protease.
1; 4DABE24D7D5BA4A4 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1
EMBL; AF198087; AAF13253.1; -.
HSSP; P00760; 1AQ7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33.0%; Score 528; DB 4 44.7%; Pred. No. 5e-44;
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                                                                                        InterPro; PR002172; LDL receptor A. InterPro; IPR001254; Ser_protease_Try. InterPro; IPR001254; Ser_protease_Try. InterPro; IPR001190; Srcr_receptor. Pfam; PF00057; Idl_recept_a; 1. Pfam; PF00089; trypsin; 1. SMART; SM00192; LDLa; 1. SMART; SM00202; SR; 1. SMART; SM00202; SR; 1. PROSITE; PS50287; SRCR_2; 1. PROSITE; PS50240; TRYPSIN DOM; 1. PROSITE; PS00134; TRYPSIN HIS; 1. PROSITE; PS00135; TRYPSIN SER; 1. Hydrolase; Protease; Serine protease. SEQUENCE 581 AA; 62689 MW; 4DABE24D7
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INTERPRO; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Tr
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN HIS; 1.
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ophys. Acta 1518
796; BAB39741.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
les 105; Conserv
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KIVGGYALDVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHCFRKHTDVFNWKVRAGSD
                                                            TPATPLWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPEG
                                                                                                                                                                                                       SIMDSPVPSHLVBKII---YHSKYKPKRLGNDIALMKLSEPLTFDETIQPICLPNSEENF
                                                                                                                                                                                                                                                                                                                                                                                                                                         GVDTCQGDSGGPLMYQSDQ-WHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKARL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KL--GSFPSLAVAKIIIIEFNPMY-PK--DNDIALMKLQFPLTFSGTVRPICLPFFDEEL
                                                                                                                                                                                                                                                                                                                                       333 PDGKLCWTSGWGAT-EDGGDASPVLNHAAVPLISNKICNHRDVYGGIISPSMLCAGYLKG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               276 SLMDSPVPSHLVEKII---YHSKYKPKRLGNDIALMKLSEPLTFDETIQPICLPNSEENF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     333 PDGKLCWTSGWGAT-EDGGDASPVLNHAAVPLISNKICNHRDVYGGIISPSMLCAGYLKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TPATPLWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAXQGEVTEKMMCAGIPEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=citb-cj7;

Guipponi M., Scamuffa N., Scott H.S., Antonarakis S.E.;

Guipponi M., Scamuffa N., Scott H.S., Antonarakis S.E.;

"Isolation of the mouse Tmprss3 genomic DNA sequence.";

Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.

-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.

EMBL; AJ429216; CAD22137.1; -.

InterPro; IPR001172; LDL receptor A.

InterPro; IPR001124; Ser_protease_Try.

R InterPro; IPR001254; Ser_protease_Try.

R InterPro; IPR001254; Ser_protease_Try.

R Pfam; PF00089; trypsin; 1.

Pfam; PF00089; trypsin; 1.

PRMRT; SM0020; SR; 1.

R SMART; SM00102; LDLa; 1.

R SMART; SM0020; SR; 1.

R SMART; SM0020; SR; 1.

R SMART; SM0020; SR; 1.

R PROSITE; PS50240; TRYPSIN DOM; 1.

R PROSITE; PS50240; TRYPSIN DOM; 1.

R PROSITE; PS00134; TRYPSIN DOM; 1.

R PROSITE; PS00134; TRYPSIN SER; 1.

R PROSITE; PS00135; TRYPSIN SER; 1.

R PROSITE; PS00135; TRYPSIN SER; 1.

R PROSITE; PS00135; TRYPSIN SER; 1.

R PROSITE; PS00135; TRYPSIN SER; 1.
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larity 44.2%; Pred. No. 1.1e-43;.
Conservative 41; Mismatches 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OBKITO;
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence up
01-MAR-2003 (TrEMBLrel. 23, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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106; Conserv
                                                                                    216
                                                                                                                                                        111
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Best Local S:
Matches 106
                   51
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P SEQUENCE FROM N.A.

Guipponi M., Scamuffa N., Scott H.S., Rossier C., Antonarakis S.E.;

T "Isolation and characterization of the mouse Tmprss3 gene.";

L Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.

- I-SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.

R BMBL; AJ300738; CAC83350.1; -.

R BMBL; AJ300751; LANI.

R BMSL; PR001114; Chymotrypsin.

R InterPro; IPR001114; Chymotrypsin.

R InterPro; IPR001125; LDL_receptor.

R InterPro; IPR001125; LDL_receptor.

R InterPro; IPR001190; Srcr_receptor.

R Ffam; PP00089; LTYPESIN.

R Pfam; PP00089; LDLa; 1.

R PRNTS; SM00192; LDLa; 1.

R PROSITE; PS50289; LDLa; 1.

R PROSITE; PS50287; SRCR_Z; 1.

R PROSITE; PS50134; TRYPSIN DOM; 1.

R PROSITE; PS00134; TRYPSIN DOM; 1.

R PROSITE; PS00135; TRYPSIN SER; 1.

R PROSITE; PS00135; TRYPSIN SER; 1.

R PROSITE; PS00135; TRYPSIN SER; 1.

R PROSITE; PS00135; TRYPSIN SER; 1.

R PROSITE; PS00135; TRYPSIN SER; 1.

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R PROSITE; PS00135; TRYPSIN SER; 1.

R PROSITE; PS00135; TRYPSIN SER; 1.

R PROSITE; PS00135; TRYPSIN SER; 1.

R PROSITE; PS00135; TRYPSIN SER; 1.

R PROSITE; PS00135; TRYPSIN SER; 1.

R PROSITE; PS00135; TRYPSIN SER; 1.

R PROSITE; PS00135; TRYPSIN SER; 1.

R PROSITE; PS00135; TRYPSIN SER; 1.

R PROSITE; PS00135; TRYPSIN SER; 1.

R PROSITE; PS00135; TRYPSIN SER; 1.

R PROSITE; PS00135; TRYPSIN SER; 1.

R PROSITE; PS00135; TRYPSIN SER; 1.
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                                                                                                                                                                                                                                                                                   14 LLLVVSNLLLCOGVVSDYKDDDDVDAAALAAPFD----DDDKIVGGYALDVDSWPWQVSI
                                                                                                                                                                                                                                                                                                                            QYDKQHVCGGSILDPHWVLTAAHCFRKHTDVFNWKVRAGSDKLGSFPSLAVAKIIII----
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                                                                                                                                                   DB 11; Length
                                                                                                                                                                                                                    96; Indels
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                                      POTENTIAL.
1C28069DF0064546 CRC64;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
Last sequence update)
Last annotation update)
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                                                                                                                                        32.9%; Score 526.5; DB 1
40.4%; Pred. No. 2.6e-44;
ive 49; Mismatches 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   276
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44.6%; Pred. No. 9e-44;
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                                                                         0522 MW;
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                                                                                                                             Query Match 32.9%
Best Local Similarity 40.4%
Matches 110; Conservative
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Q8VDEO;
01-MAR-2002 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
TMPRSS3 protein.
TMPRSS3.
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Hydrolase, Protease,
SIGNAL 1
SEQUENCE 279 AA;
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Best Local Similarity
Matches 107; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124
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107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G---SDKLGSFPSLAVAKIIIIEFNPMYPKDN---DIALMKLQFPLTFSGTVRPICLPFF 161
LMYQSDQ-WHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL 284
              309 YLDGRADACQGDSGGPLVCPSGDTWHLVGVVSWGRGCAEPNRPGVYAKVAEFLDWIHD 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGGPLMYQS-DQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYN 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51 KIVGGYALDVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHC---FRKHTDVFNWKVRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OBCUL7

OBCUL7

OBCUL7

OLAMA-2003 (TrEMBLrel. 23, Created)

OL-MAR-2003 (TrEMBLrel. 23, Last sequence update)

OL-MAR-2003 (TrEMBLrel. 23, Last annotation update)

OL-MAR-2003 (TrEMBLrel. 23, Last annotation update)

Adrenal mitochondrial protease long variant.

AMP.

Rattus norvegicus (Rat).

Rattus norvegicus (Rat).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

NCBI TaxID=10116;
                                                                                                                                                                                                               Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 11; Length 445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A.B., Lowry P.J.;
f a rat adrenal mitochondrial protease.";
02) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                        ., Lowry P.J.;
rat adrenal mitochondrial protease.";
to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             82; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48440 MW; BE3F56D8372ED988 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                  40694 MW; 89A64081D9A1FE26 CRC64;
                                                                                                     OBCJ16 PRELIMINARY; PRT; 371 AA.
OBCJ16;
O1-MAR-2003 (TrEMBLrel. 23, Created)
O1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
O1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Adrenal mitochondrial protease short variant.
                                                                                                                                                                                                                                                                                                                                                                                                                              32.6%; Score 522; DB 11;
42.0%; Pred. No. 1.1e-43;
ive 42; Mismatches 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32.6%; Score 522;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=NEDH;
OMER S., Bicknell A.B., Lowry
"Identification of a rat adres
Submitted (AUG-2002) to the E
EMBL; AF537098; AAN06757.1;
Protease.
SEQUENCE 445 AA; 48440 MW;
                                                                                                                                                                                                                                                                                                                      Omer S., Bicknell A.B., Lowr "Identification of a rat adr Submitted (AUG-2002) to the EMBL; AF537099; AAN06758.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             100; Conservative
                392 GVDSCQGDSGGPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPEGGVDTCOGD
GVDTCQGDSGGP
                                                                                                                                                                                                                                                                                                                                                                                                 371 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                          FROM N.A
                                                                                                                                                                                                                                                            NCBI TaxID=10116;
                                                                                                                                                                                                                                                                                                           STRAIN=NEDH
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 100
                                                                                                                                                                                                                                                                                                                                                                                    Protease.
SEQUENCE
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226
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8CJ17
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8CJ16
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                                                                                                                                                                                                                                                                                        266 GLVSHSAVRQHQGTMVEKIIP---HPLYSAQNHDYDVALLQLRTPINFSDTVSAVCLPAK 322
                                                                                                                                                                                                                                                                                                                                                                                                                    323 BQHFPQGSQCWVSGWGHTDPSHTHSSDTLQDTMVPLLSTDLCNSSCMYSGALTHRMLCAG 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           110 DKLGSFPSLA---VAKIIIIEFNPMYPKDNDIALMKLOFPLTFSGTVRPICLFFFBELT 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 590 LTKPSYYNASAYFVERIIVHPGYKSYTYDNDIALMKLRDEITFGYTTQPVCLPNSGMFWE 649
                                                                                                                           51 KIVGGYALDVDSWFWQVSIQYDKQHVCGGSILDPHWVLTAAHC---FRKHTDVFNWKVRA 107
                                                                                                                                                                                                                                                     108 G---SDKLGSFPSLAVAKIIIIEFNPMYPKDN---DIALMKLQFPLTFSGTVRPICLPFF 161
                                                                                                                                                                                                                                                                                                                                                                                DEBLTPATPLWIIGWGFTKONGGKWSDILLOASVQVIDSTRCNADDAYQGEVTEKWWCAG 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          222 IPEGGVDTCQGDSGGPLMYQS-DQMHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYN 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             383 YLDGRADACQGDSGGPLVCPSGDTWHLVGVVSWGRGCAEPNRPGVYAKVAEFLDWIHD 440
                                                                                                                                                            51 KIVGGYALDVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHC-FRKHTDVFNWKVRAGS
                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=20363741; PubMed=10903452;
Yamada K., Takabatake T., Takeshima K.;
"Isolation and characterization of three novel serine protease genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xenopus laevis (African clawed frog).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus.
                                                          14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
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InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001354; Ser_protease_Try.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00122; CHYMOTRYPSIN.
SMART; SM00192; LDLa, 8.
SMART; SM00192; LDLRA : 8.
SMART; SM00192; LDLRA : 8.
PROSITE; PS01089; LDLRA 1; 8.
PROSITE; PS01039; LDLRA 1; 2.
PROSITE; PS00139; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
Hydrolase; Protease; Serine protease.
SEQUENCE 767 AA; 86001 MW; E0566A38796DE96E CRC64;
                           Pred. No. 1.4e-43;
; Mismatches 82; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Embryonic serine protease-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32.6%; Score 522; DB 13;
44.2%; Pred. No. 2.9e-43;
:ive 40; Mismatches 84;
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Gene 252:209-216(2000).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY
EMBL; AB038497; BAB08217.1;
HSSP; P00766; 1CHG.
MEROPS; S01.049; -.
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42.0%; FIL.
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Best Local Similarity 44.2°
Matches 103; Conservative
                                                            100; Conservative
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                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=8355;
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                                                            Matches
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                                                                                                                                                                                                                                                                                                                                   =Trachea;
t M., Hammer F., Schammann M., Allolio B.;
rization of RAT, the airway trypsin-like protease
        TKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPEGG
                       650 AGTITWISGWGSTYB-GGSVSTYLQYAAIPLIDSNVCNQSYVYNGQITSSMICAGYLSGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TPATPLWIIGWGFTKONGGKMSDILLOASVQVIDSTRCNADDAYQGEVTEKWMCAGIPBG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49 DDKIVGGYALDVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHCFRKHTDVFNWKVRAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SDKLGSFPSLAVAKIIII----EFNPMYPKDNDIALMKLOFPLTFSGTVRPICLPFFDEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       300 MPDSVAXVTGWGSLTYGGNTVTN-LQQGEVRIVSSEVCNEPAGYGGSVLPGMLCAGVRSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               243 VSTIS--PRLRVRVRAILAHAEYNSI-TRDNDIAVVQLDRPVTFTRNIHRVCLPAATQNI
                                                                                                                                                                                                                                                                  Euteleostomi;
Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   276
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                                                                            VDTCQGDSGGPLVNKRNGTWWLVGDTSWGDGCARANKPGVYGNVTTFLEWIYS
                                                             VDTCQGDSGGPLM-YQSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12.6%; Score 521.5; DB 11; Length
12.1%; Pred. No. 1.4e-43;
.ve 44; Mismatches 82; Indels
                                                                                                                                                                                                                                                                                                                                                                                             databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB9504158B018E21 CRC64;
                                                                                                                                                                                                                                                               Craniata; Vertebrata; E
Sciurognathi; Muridae;

    20, Created)
    20, Last sequence update)
    23, Last annotation update)

rotease.
                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=Wistar; TISSUE=Trachea;
A Hansen I.A., Fassnacht M., Hammer F., Schammann M.,
T "Cloning and characterization of RAT, the airway t:
    "Cloning and characterization of RAT, the airway t:
    "Cloning and characterization of RAT, the airway t:
    "Cloning and characterization of RAT, the airway t:
    "Cloning and characterization of RAT, the airway t:
    "I chartus norvegicus.";
    Submitted (NOV-2001) to the EMBL/GenBank/DDBJ data
    "Cloning and characterization of RAT, the airway t:
    "Submitted (NOV-2001) to the EMBL/GenBank/DDBJ data
    "FRSP, PO0761; 1ANI.
    "REMBL, AF453776; AAL50817.1; -
    "REMBL; AF453776; AAL50817.1; -
    "REMBL; AF453776; AAL50817.1; -
    "REMPLY STRAINS SEA, 1.
    "REMPLY STRAINS SEA, 1.
    "PEAM; PF00089; trypsin; 1.
    "PEAM; PF00089; trypsin; 1.
    "PTNTS; PR00722; CHYMOTRYPSIN.
                                                                                                                                                                  417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PRO012; CHYMOTRYPSIN.
SMART; SM00020; SEA; 1.
PROSITE; PS50024; SEA; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
Hydrolase; Protease; Serine protease.
SEQUENCE 417 AA; 46287 MW; DB950415
                                                                                                                                                                                                                                                              hordata; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 42.18
Matches 98; Conservative
                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                          Q8VHJ4;
01-MAR-2002 (TYEMBLrel.
01-MAR-2002 (TYEMBLrel.
01-MAR-2003 (TYEMBLrel.
Airway trypsin-like prof
Rattus norvegicus (Rat)
Eukaryota; Metazoa; Choj
Mammalia; Butheria; Rode
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      PATPLWIIGWGF'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              226 GVDTCQGDSGGPI
      167
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98CDR0
D Q8CDR0
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8VHJ4
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PRELIMINARY;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 276 GLVSHGAVRQHQGTMVEKIIP---HPLYSAQNHDYDVALLQLRTFINFSDTVGAVCLPAK 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                222 IPEGGVDTCQGDSGGPLMYQS-DQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYN 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51 KIVGGYALDVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHC---FRKHTDVFNWKVRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        108 GSDKLGS---FPSLAVAKIIIIEFNPMYPKDN---DIALMKLOFPLTFSGTVRPICLPFF
                                                                                                                                                                                                                                                                                                                                                                           STRAIN=C57BL/6J; TISSUB=Testis;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
EMBL; AK029714; BAC26577.1; -.
EMBL; AK029714; BAC26577.1; -.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32.4%; Score 519; DB 11; Length 455; ilarity 42.4%; Pred. No. 2.9e-43; Conservative 41; Mismatches 82; Indels 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  databases
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01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to airway trypsin-like protease.
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Strausberg R.;
Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ dat.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.
EMBL; BC020151; AAH20151.1; -.
HSSP; P00761; 1AM1.
MEROPS; S01.047; -.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; SEA_domain.
InterPro; IPR001254; SEA_domain.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF01390; SEA; 1.
Pfam; PF01390; SEA; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00200; SEA; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence up
01-MAR-2003 (TrEMBLrel. 23, Last annotation
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                                                                                                                     Transmembrane protease. Mus musculus (Mouse).
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Best Local Similarity
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SDKLGSFPSLAVAKIIIIEFNPMYPKDNDIALMKLOFPLTFSGTVRPICLPFFDEELTPA 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tidentification and localization of MAT - the murine homologue of the human airway trypsin-like protease (HAT).";

L'almited (NOV-2001) to the EMBL/GenBank/DDBJ databases.

L'similarity EBELONGS TO PEPTIDASE FAMILY SI.

EMBL; AF448809; AAL47139.1; -.

R HSSP; POO761; IANI.

R HSSP; POO761; IANI.

R HSSP; POO161; IANI.

R HSSP; POO162; AAL47139.1; -.

R HSSP; POO162; AAL47139.1; -.

R HSSP; POO162; AAL47139.1; -.

R HSSP; POO162; AAL47139.1; -.

R HSSP; POO162; AAL47139.1; -.

R HSSP; POO162; AAL47139.1; -.

R PRO0139; SEA; I.

R PRON175; PRO01254; SEA; I.

R PROSITE; PSSO024; SEA; I.

R PROSITE; PSSO024; SEA; I.

R PROSITE; PSSO0134; TRYPSIN HIS; I.

R PROSITE; PSO0135; TRYPSIN HIS; I.

R PROSITE; PSO0135; TRYPSIN HIS; I.

R HYDROLASE; Protease; Serine protease.

Q SEQUENCE 417 AA; 46220 MW; 631ACF83C62DEBIE CRC64;
                                                                                                                                                                                                                        49 DDKIVGGYALDVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHCFRKHTDVFNWKVRAG
                                                                                                                                                                                                                                                               243 VSTMSPRLRVRVRAILAHDGYSSVTRDNDIAVVQLDRSVAFSRNIHRVCLPAATQNIIPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     362 ACQGDSGGPLVQEDSRRLWFVVGIVSWGYQCGLPNKPGVYTRVTAYRNWI 411
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                                                                                                  DB 11; Length 417;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCQGDSGGPLMYQSDQ--WHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWI
                                                                                          31.8%; Score 509.5; DB 11; Length
40.4%; Pred. No. 2.3e-42;
ive 42; Mismatches 92; Indels
    ; Serine protease.
46254 MW; C7FACD21C06FEAEA CRC64;
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.. 20, Last sequence update)
.. 23, Last annotation update)
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Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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Matches 93; Conservative
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OBVHK8;

01-MAR-2002 (TrEMBLrel.

01-MAR-2003 (TrEMBLrel.

01-MAR-2003 (TrEMBLrel.
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Hydrolase; Protease;
SEQUENCE 417 AA;
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MODEL=frame+ p2n.model -DEV=xlh
Q=/cgn2_1/USPTO_spool/US09607745/runat_21112003_144345_22184/app_query.fasta_1.1038
DB=GenEmbl -OFWT=fastap -SUFFIX=rge -MINMATCH=0_1 -LOOPCL=0 -LOOPEXT=0
UNITS=bits -START=1 -BND=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
UNITS=bits -START=1 -THR_SCORE=pct -THR_MAX=100 -THR_NIN=0 -ALIGN=15 -MODE=LOCAL
DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -MAXLEN=2000000000
USER=US09607745_@CGN 1 15308_@runat_2112103 144345_22184 -NCPU=6 -ICPU=3
NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                            2003, 07:52:05; Search time 3687.55 Seconds (without alignments) 3239.440 Million cell updates/sec
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1 MDSKGSSQKSRLLLLLLVVSN......LNWIYNVWKAELSRHHHHH
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Compugen Ltd.
                                                      using frame_plus_p2n model
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 24 Row: m Column: 19.

Location/Qualifiers
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Submitted (15-AUG-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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/clone_lib="NIH_MGC_39"
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ICLPFFDEELTPATPLWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGBV
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                                                                 Corley, N.C.
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Mismatches:
Indels:
Gaps:
Unknown.

SM Unknown.

Unclassified.

JORS Bandman,O., Hillman,J.L., Yue,
Tang,Y.Tom. and Shah,P.
Human protease molecules
Patent: US 6203979-A 18 20-MAR-2001;
Location/Qualifiers

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'organism="unknown"
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Baton,D.L., Filvaroff,E., Gerritsen,M.E., Goddard,A.,
Godowski,P.J., Grimaldi,C.J., Gurney,A.L., Watanabe,C.K. and
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Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Genentech, Inc. (US)
Location/Qualifiers
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Sequence 111 from Patent WO0116318.
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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Human protease molecule.

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Home sapiens

Home sapiens

Chordata; Craniata; Vertebrata; Buteleostom;

Mammalia; Butheria; Primates; Catarrhini; Hominidae, Homo.

CE I (Pases 1 to 2038)

RS Bandman, J.L., Yue, H., Guegler, K.J., Corley, N.C.,

Tang, T.Y. and Shah, P.

Human protease molecule

NoryTE PHARMACEUTICALS INC

OS Homo sapiens (human)

PD 26-MAR-2002

PF 12-JAN-1999 UP 2000540252

PF 12-JAN-1999 US 09/008271

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PI TOM Y TANG, PURVI SHAH

PC C1201/68, C1201/68, C1201/201/21, C1201/21, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/68, C1201/
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PN JP 2002508970-A/6
PD 26-MAR-2002
PF 12-JAN-1999 US 09/008271
PI OLGA BANDMAN, JENNIFER L HILLMAN, HENRY YUE, KARL J GUEGLER, NEII
PI C CORLEY,
PI TOM Y TANG, PURVI SHAH
PC C12N15/09, A61K38/46, C07K16/40, C12N1/19, C12N1/21, C12N5/10 PC, C12N9/48, C12N9/64,
PC C12N9/48, C12N9/64,
PC C12N9/68, C12N15/00, A61K37/54, C12N5/00
CC 1337018
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Location/Qualifiers

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/organism='Homo sapiens (human)'.

/organism="Homo sapiens"
/mol_type="genomic DNA"
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Goddard, A., Godowski, P.J., Gurney, A.L., Hillan, K.J., Polakis, P.,
Smith, V., Wood, W.I., Wu, T.D. and Zhang, Z.
Compositions and methods for the diagnosis and treatment of tumo
Patent: WO 0216429-A 2 28-FBB-2002;
Genentech, Inc. (US)
Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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S Baker, K.P., Chen, J., Desnoyers, L., Goddard, A., Godowski, P.J.,
Gurney, A.L., Pan, J., Smith, V., Watanabe, C.K., Wood, W.I. and
Zhang, Z.
Secreted and transmembrane polypeptides and nucleic acids encoding
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L Patent: WO 0168848-A 329 20-SEP-2001;
Genentech, Inc. (US)

Genentech, Inc. (US)

1. 2063

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Eaton,D.L., Gao,W.Q., Pan,J., Botstein,D., Fong,S., Goddard,A.,
Godowski,P.J., Gurney,A.L., Smith,V., Tumas,D., Wood,W.I.,
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Methods of diagnosing colorectal cancer, compositions, of screening for colorectal cancer modulators
Patent: US 6455668-A 1 24-SEP-2002;
Location/Qualifiers
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Nucleic acid molecules encoding transmembrane serine proteases, encoded proteins and methods based thereon Patent: WO 0157194-A 71 09-AUG-2001; CORVAS INTERNATIONAL, INC. (US)
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151 GlyThrValArgProIleCysLeuProPhePheAspGluGluLeuThrProAlaThrPro 170 1118 GGCACAGTCAGGCCCATCTGCTCTTTGATGAGGAGCTCACTCCAGCCACCCA 1177 171 LeuTrpileIleGlyTrpGlyPheThrLysGlnAsnGlyGlyLysMetSerAspIleLeu 190 172 LeuGlnAlaSerValGlnValIleAspSerThrArgCysAsnAlaAspAspAlaTyrGln 210 173 CTGCAGGCTCAGTCCAGTCATTGACAGCACACGGTGCAATGCGACGATGCGTACTG 1237 174 LeuGlnAlaSerValGlnValIleAspSerThrArgCysAsnAlaAspAspAlaTyrGln 210 175 CTGCAGGCGTCAGTCCAGTCATTGACAGCACACGGTGCAATGCGATGCGTACCAG 1297 176 CTGCAGGCGTCAGTCCAGTCATTGACAGCACACGGTGCAATGCAGACGATGCCTACCAG 1297 177 GlyGluValThrGluLysMetMetCysAlaGlyIleProGluGlyGlyValAspThrCys 230	ы го 44 г 44	AF216312  Homo sapiens type II membrane serine protease mRNA, complete cds.  AF216312.1 GI:6911218  Homo sapiens (human)  Homo sapiens  Homo sapiens  Homo sapiens  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  1 (bases 1 to 2079)  Smeekens, S.S., Lorimer, D.D., Wang, E., Hou, J. and Linnevers, C.  MT-SP2, a novel type II membrane serine protease expressed in trachea, colon, and small intestine: identification, cloning, and	Chromosomal localization Unpublished 2 (bases 1.02079) 2 (bases Lozimer, D.D., Wang, E., Hou, J. and Linnevers, C. Direct Submission Submitted (14-DEC-1999) Axys Pharmaceuticals, Inc, 180 Kimball Way, South San Francisco, CA 94080, USA Location/Qualifiers 1. 2079   /organism="Homo sapiens" / mol_type="mRNA" / db_xref="taxon:9606" / con 251. 1522 / con 252.	/ noce="MI-SEZ" / codon_start=" / product="type II membrane serine protease" / product="type II membrane serine protease" / protein_id="AAF31436.1" / db_xref="G1:6911219" / translation="MSNPCANPVSPWRPSESVGIPIIIALLSLASIIIVVVLIKVILD KYYFLCGQPLHFIPRKQLCDGELDCPLGEDBEHCVKSFPEGPAVAVRLSKDRSTLQVL DSATGNWFSACFDNFTEALAETACRQMGYSSKPTFRAVEIGPDQDLDVVEITENSQEL RMRNSSGPCLSGSLVSLHCLACGKSLKTPRVVGGEEASVDSWPWQVSIQYDKQHVCGG SILDPHWVLTAAHCFRKHTDVFNWKVRAGSDKLGSFPSLAVAKIIIIEFNPMYPKDND IALMKLQFPLTFSGTVRPICLPFFDEELTPATPLWIIGWGFTKQNGGKMSDIILQASV QVIDSTRCNADDAYQGEVTEKMMCAGIPEGGVDTCQGDSGGPLMYQSDQWHVVGIVSW GYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL"  489 a 594 c 575 g 421 t
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                                                                                                                1CysGlyGlySerIleLeuAspProHisTrpValLeuThrAla
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Homo sapiens, Similar to mosaic serine protease, clone MGC:19490 IMAGE:3610695, mRNA, complete cds.
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BC011703.1 GI:15079794
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1 (bases 1 to 2088)

Strausberg, R.

Direct Submission
Submitted (30-JUL-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
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pancreatic cancer
Cancer Res. 60 (10), 2602-2606 (2000)
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2 (bases 1 to 2081)
Wallrapp,C. and Gress,T.M.
Direct Submission
Submitted (20-AUG-1999) Internal Medicine I, University of Ulm, Robert-Koch-Street 8, Ulm, Baden-Wuerttemberg 89081, Germany
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Human cDNA encoding a serine protease.

E13203

E13203

E13203.

E13203.1 GI:3252008

JP 1997149790-A/4.

Homo sapiens (human)

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleo Mammalia; Pthheria; Primates; Catarrhini; Hominidae; Homo.

Tsuruoka,N., Yamashiro,K., Tsujimoto,M. and Yamaguchi,M.

NEW SERINE PROTEASE

Patent: JP 1997149790-A 4 10-JUN-1997;

SUNTORY LTD
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VIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact:
Netherby, K.D., Beckstrom-Sternberg, S.M.,
Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S.,
Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Legaspi, R.,
Lim, M., Maduro, Q.L., Masiello, C., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Snyder, B., Stantripop, S., Thomas, P.J.,
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 8347148.

Location/Qualifiers

1. 2088

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| /lab host="DH10B-R" |
| /note="Vector: pOTB7" |
| /note="Vector: pOTB7" |
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RS Suendermann, B., Hofmann, U., Matzku, S. and Wilbert, O.

Seripancrin

[AL Patent: WO 0104141-A 3 18-JAN-2001;

MERCK PATENT GmbH (DE)

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	14	1266	79	2063	25	ACA60418	Novel human secret
	15	1266	79	2063	25	ACA63428	cDNA encoding huma
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	20	1266	7.9	2063	25	ABX78692	Human PRO polynucl
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	56	1266	79	2079	25	ABS57763	cDNA encoding huma
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3	Homo	o sapiens	ns.				

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Nucleic acid encoding a serine protease called D-G protein which useful for identifying modulators that are useful for treating a condition which is mediated by protease D-G, e.g. cancer, skin disorders, or neuropathic pain -
             13..891
/*tag= a
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/transl_except= (pos: 640..642, aa
13..93
/*tag= b
/note= "Prolactin signal sequence"
94..888
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/note= "Mature protease D-G"
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The invention relates to an isolated and purified nucleic acid that encodes a serine protease called D-G protein. The activity of the protein of the invention may be described as cytostatic, antiinflammatory, dermatological and anticoagulation. The serine protease of the invention is a member of the trypsin/chymotrypsin-like (SI) serine protease family, which play an important role in processes such as digestion and regulatory amplification cascades through the proteolytic activation of inactive zymogen precursors. Protease D-G modulating compounds are useful for treating a condition which is mediated by protease D-G, e.g. cancer, skin disorders, neuropathic pain, inflammatory disorders, or coagulation diathesis/thrombosis. The polymolectide encoding the protease is useful for identifying, detecting or isolating mutant forms of DNA molecules encoding the protease. The D-G protein can be used for formulation of compositions for laundry detergents and skin care products. Protease C-G gene therapy may be used to introduce protease D-G into the cells of target organisms. As the D-G protein is derived from a human, it is less likely to produce an allergic reaction in sensitive individuals when used in formulations for laundry detergents and skin care products. The current sequence represents the protease D-G cataytic domain in the construct encoding sequence

G; 280 T; 0 other; C; 307 A; 305 297 BP; Sequence 1189

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MetAspSerLysGlySerSerGlnLysSerArgLeuLeuLeuLeuValValSerAsn
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        Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                            133 GCTCTTGCTGCCCCCTTTGATGATGATGACAAGATCGTTGGGGGCTATGCTCTAGATGTG
                                                                    AspSerTrpProTrpGlnValSerIleGlnTyrAspLysGlnHisValCysGlyGlySer
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sis, arthritis, chronic obstructive pulmonary disease,
story disorders, stroke, angiogenesis and aberrant
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 Location/Qualifiers
1..1305
/*tag= a
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/note= "The coding region does not include stop of partial
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P-PSDB; AAY72558.
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AAACTGGGCAGCTTCCCATCCCTGGCTGTGGCCAAGATCATCATCATCATTGAATTCAACCCC
                                                GlyThrValArgProlleCysLeuProPhePheAspGluGluLeuThrProAlaThrPro
                                                                                                                                                                               GGCACAGTCAGGCCCATCTGCTGCCCTTCTTTGATGAGGAGCTCACTCCAGCCACCCCA
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                                   MetTyrProLysAspAsnAspIleAlaLeuMetLysLeuGlnPheProLeuThrPheSer
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; 2001US-290492P.
; 2001US-339245P.
; 2001US-350666P.
; 2001US-334370P.
; 2002US-372246P.
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P-PSDB; ABU56625.
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12-APR-2002;
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Detecting a lung cancer-associated transcript in a cell from a patient for treating lung cancer, by contacting a biological sample from the patient with a polynucleotide that exhibits increased or decreased expression in lung cancer - Claim 22; Page 353; 453pp; English.

The invention relates to a method for detecting a lung cancer-associated transcript in a cell from a patient, comprising contacting a biological sample from the patient with a polynuclectide that selectively hybridises to a sequence that is at least 80 % identical to a gene that exhibits increased or decreased expression in lung cancer samples. Lung cancer-associated polynuclectides and polypeptides are used for identifying a compound that modulates a lung cancer-associated polynuclecting proliferation of a lung cancer-associated polypeptide, for inhibiting proliferation of a lung cancer-associated cell to treat lung cancer in a patient and for treating a mammal having lung cancer by administering a modulatory compound identified. The methods are useful for treating lung cancer, such as small cell lung cancer or other benign or precancerous lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and bronchiectasis. The genes, polynucleotides are useful for diagnostic purposes and as targets for screening for therapeutic compounds that modulate lung cancer, such as antibodies. Sequences ABX76124-ABX76474 represent lung cancer-associated polynucleotides of the invention.

Sequence 1314 BP; 297 A; 369 C; 373 G; 275 T; 0 other;

GlyGluValThrGluLysMetMetCysAlaGlyIleProGluGlyGlyValAspThrCys LysllevalGlyGlyTyrAlaLeuAspvalAspSerTrpProTrpGlnValSerIleGln TyrAspLysGlnHisValCysGlyGlySerIleLeuAspProHisTrpValLeuThrAla ProlleCysLeuProPheAspGluGluLeuThrProAlaThrPro LeuTrpileIleGlyTrpGlyPheThrLysGlnAsnGlyGlyLysMetSerAspileLeu /alGlnValIleAspSerThrArgCysAsnAlaAspAspAlaTyrGln CTGCAGGCGTCAGTCCAGTCATTGACAGCACACGCTGCAATGCAGACGATGCGTACCAG 366GAGGAGGCCTCTGTGGATTCTTGGCCTTGGCAGGTCAGCATCCAG rgLysHisThrAspValPheAsnTrpLysValArgAlaGlySerAsp AGGAAACATACCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGAC spasnaspilealaLeuMetLysLeuGlnPheProLeuThrPheSer LysteuGlySerPheProSerLeuAlaValAlaLysIleIleIleIleGluPheAsnPro CCCATCTGTCTGCCCTTCTTTGATGAGGAGCTCACTCCAGCCACCCCA 1314 228 4 0 Length:
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Human; cancer; ulcer; HIV infection; human immunodeficiency virus; antiinflammatory; antirheumatic; antiarthritic; immunosuppressive; antiinflammatory; antirheumatic; antiardemic; anaemia; antiagregant; haemostatic; vulnerary; antialcer; osteopathic; eczema; dermatological; antiallergic; antiasthmatic; antidabetic; cytostatic; wheuroprotective; antidepressant; nootropic; antiparkinsonian; infection; meuroprotective; antidepressant; nootropic; antiparkinsonian; infection; meuroprotective; rheumatoid arthritis; septic shock; pancreatitis; antiamaphylactic; rheumatoid arthritis; septic shock; pancreatitis; cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity; genetic disease; haematopoietic disorder; platelet disorder; asthma; allergic rhinitis; diabetes; multiple sclerosis; depression; allergic rhinitis; disbetes; multiple sclerosis; depression; multiple sclerosis; depression; multiple sclerosis; depression; multiple sclerosis; depression; multiple sclerosis; depression; multiple sclerosis; depression; multiple sclerosis; depression; multiple sclerosis; depression; multiple sclerosis; depression; multiple sclerosis; depression; multiple sclerosis; depression; multiple sclerosis; depression; multiple sclerosis; depression; multiple sclerosis; depression; multiple sclerosis; depression; multiple sclerosis; depression; multiple sclerosis; depression; multiple sclerosis; depression; multiple sclerosis; depression; multiple sclerosis; depression; multiple sclerosis; depression; multiple sclerosis; depression; multiple sclerosis; depression; multiple sclerosis; depression; multiple sclerosis; depression; multiple sclerosis; depression; multiple sclerosis; depression; multiple sclerosis; depression; multiple sclerosis; depression; multiple sclerosis; depression; multiple sclerosis; depression; multiple sclerosis; depression; multiple sclerosis; depression; multiple sclerosis; depression; multiple sclerosis; depression; multiple sclerosis; depression; multiple sclerosis; depression; multiple sclerosis; 270 AAH99166 to AAH99904 encode the human proteins given in AAM25225 to AAM25963. The proteins can have activities based on the tissues and cells they are expressed in, such as: antiinflammatory; antirheumatic; antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant; central nervous system; virucide; anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; antiaggregant; haemostatic; vulnerary; antiulcer; osteopathic; dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic; GlnGlyAspSerGlyGlyProLeuMetTyrGlnSerAspGlnTrpHisValValGly1le CAGGGTGACAGTGGGCCCCTGATGTACCAATCTGACCAGTGGCATGTGGTGGGCATC GITAGCTGGGGCTATGGCTGCGGGGGCCCCGAGCACCCCCAGGAGTATACACCAAAGGTCTCA ValSerTrpGlyTyrGlyCysGlyGlyProSerThrProGlyValTyrThrLysValSer polypeptides, useful for ulcers and HIV infection 284 AlaTyrLeuAsnTrpIleTyrAsnValTrpLysAlaGluLeu GCCTATCTCAACTGGATCTACAATGTCTGGAAGGCTGAGCTG Human protein encoding cDNA sequence SEQ ID NO:409. Isolated human polynucleotides encoding treatment and diagnosis of e.g. cancer, 506; 1217pp; English. g B standard; cDNA; 1854 RT 22-DEC-2000; 2000WO-US35017. 23-DEC-1999; 99US-0471275. 21-JAN-2000; 2000US-0488725. 25-APR-2000; 2000US-0552317. Drmanac (first WPI; 2001-457603/49. P-PSDB; AAM25633. (HYSE-) HYSEQ INC ပဲ WO200153455-A2 Liu Claim 1; Page 16-OCT-2001 26-JUL-2001 1150 1210 271 1270 AAH99574/c ID AAH99574 AAH99574; 251 1090 231 Tang YT, g g Š

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antiparkinsonian; and immunostimulant. The proteins and polynucleotides encoding them can be used in gene therapy, antisense therapy and vaccine production. The proteins and polynucleotides are useful for screening for agonists or antagonists of a protein and for the treatment and diagnosis of disorders associated with the activity of a protein e.g. inflammation, rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction, neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal infections, autoimmunity, genetic diseases, haematopoietic disorders, anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers, osteoporosis, severe combined immunodeficiency, eczema, allergic rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression, Alzheimer's disease, Parkinson's disease, neurodegenerative and
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This nucleotide sequence codes for HUPM-6 (see AAY06437), a novel human protease. HUPM-6 cDNA was initially identified in Incyte Clone 1337018 from the colon cDNA library CoLNNOT13 using a computer search for amino acid sequence alignments. The present sequence is a consensus sequence derived from overlapping and/or extended nucleic acid sequences: Incyte Clones 1271725 (TESTTUT02), 1337018, 586982 and 588598 (UTRSNOT01). A fragment comprising nucleotides 900-949 of the present sequence can be used for hybridisation. This sequence encompasses an active site residue. Northern analysis shows expression of HUPM-6 in gastrointesinal, and male an female reproductive cDNA libraries. Approximately 65% of these libraries are associated with neoplastic disorders, and 22% with the immune response. The invention provides 12 new human proteases, i.e. HUPM-1 to -12 (see AAY06432-43), and the polynucleotides encoding them (see AAX87149-60). Also provided are vectors, host cells and methods for producing HUPM polypeptides, as well as agonists and antagonists of HUPM. Methods for treating or them are allowed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel human protease molecules useful in the treatment developmental disorders and/or cancers
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P-PSDB; AAY06437.
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Best Local Similarity:
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screening;
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Wood Ŗ, Watanabe > Smith Ā Gurney WPI; 2000-237871/20 P-PSDB; AAY99417. Goddard Baker K,

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pp; English Fig 155; 773 2; Claim

New mammalian DNA sequerreted PRO polypept: small molecule inhibit

uences encoding transmembrane, receptor or ides, useful for screening of potential peptide or tors of the relevant receptor/ligand interactions

The AAA37022 to AAA37144 encode the new isolated human transmembrane, receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The transmembrane and receptor PRO proteins can be used for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions. The polypeptides and nucleotide sequences encoding then have various industrial applications, including uses as pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR primers and hybridisation probes used in the isolation of the PRO polypeptides from the present invention.

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Homo
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PRO proteins can be used to determine the presence of tumours and also susceptibility to tumour development, particularly adrenal, lung, colon, breast, prostate, rectal, cervical, or liver tumours, in mammalian subjects. The oligonucleotide probes specific for the PRO nucleic acids can be used for genetic analysis of individuals with genetic disorders.
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GCCCACTGCTTCAGGAACATACCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGAC
                                                                  GlyThrValArgProlleCysLeuProPhePheAspGluGluLeuThrProAlaThrPro
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20-JUL-1999; 99US-0144758.
26-JUL-1999; 99US-0145698.
01-SEP-1999; 99US-0162506.
30-NOV-1999; 99WO-US28313.
02-DEC-1999; 99WO-US28551.
16-DEC-1999; 99WO-US28551.
16-DEC-1999; 99WO-US28551.
06-JAN-2000; 2000WO-US00219.
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18-FEB-2000; 2000WO-US0;

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                                                                                                                                                                                                                                                                                                    Human, ss, gene, secreted protein, transmembrane protein, antirhe antiarthritic, osteopathic, sports-related joint problem, articular cartilage defect, osteoarthritis, rheumatoid arthritis
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                                            rreuAsnTrplleTyrAsnValTrpLysAlaGluLeu
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                                                                                            brane proteins and nucleic acids designated PRO, on probes, in chromosome and gene mapping and gene
                                                                                                                                                                                               The present invention relates to secreted and transmembrane proteins. These proteins and the DNA encoding them may be used as hybridization probes, in chromosome and gene mapping and in the generation of anti-sense RNA and DNA. They may also be used used to generate either transgenic animals or knockout animals which are in turn useful for development and screening of therapeutically useful reagents. The nucleic acids may also be used in gene therapy.
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                                                                                        Secreted and transmembrane
useful as hybridization pro
therapy -
 MA,
Pan J, Paoni NF, Roy
Watanabe CK, Williams
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The invention relates to an isolated secreted and renamembrane PRO polypeptide having 80% sequence identity to a sequence appearing as ABG58581-ARG59540 or their associated signal peptide. Or a sequence of an extracellular domain of the proteins with their associated signal peptide or lacking its associated signal peptide. Also included are newtracellular domain of the proteins with their associated signal peptide of a proteins, vetors, host cells, this calds encoding the proteins and antihodise which specifically bind to the proteins. The proteins are useful for detecting a polypeptide designated as A, B, C or D in a sample suspected of containing an A, B, C or D polypeptide, or D in a sample suspected of containing the formation of the compage is indicative of the presence of an A, B, C or D polypeptide, or D/I polypeptide conjugate in the sample where A is a PRO1072 polypeptide, B is a PRO2040 polypeptide, In the Sample where A is a PRO1072 polypeptide, B is a PRO5010 polypeptide, H is a PRO5050 polypeptide, D is a PRO3070 polypeptide, In the Sample comparises a cell suspected of expressing the A, B, C or D polypeptide, The E, P, G, H or I polypeptide is labeled with a detectable label or is attached to a soil susport. The proteins are polypeptide, and a store of the A, B, C or D or E, P, G, H or I. The bioactive molecule is a toxin, a radiolabel or an antibody. The bioactive molecule as a toxin, a radiolabel or an antibody. The bioactive molecule against them are useful for modulating a biological activity of a cell expressing a polypeptide designated as A, B, C or D or E, P, G, H or I, or antibodies adminst them are useful for modulating a biological activity of a cell expressing a polypeptide designated as A, B, C or D or E, P, G, H, or I. The cell is killed. The proteins are useful for identifying and as a toxin, a radiolabel or a modulating a biological activity of a cell expressing a polypeptide designated as A, B, C or D or E, P, G, H, or I. The cell is killed. The proteins are useful for protein are 
                         9pp; English
                                                                    The invention relates
                           390
                           111;
                       Fig
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A; 591 C; 576 G; 419 T; 0 other; 2063 BP; 477 Sequence

			70	863	90	923	110	983	130	1043
			eGln	CCAG	rAla	GGCA	rAsp	AGAC	nPro	
			Seril	AGCAI	LeuTh	CTCAC	Glyse	GGCTC	PheAs	TTCAA
			lnVal	AGGTC	rpval	GGGTC	rgAla		leglu	TTGAA
	2063 228 228 000 000		LysileValGlyGlyTyrAlaLeuAspValAspSerTrpProTrpGlnValSerIleGln	IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	TyrAspLysGlnHisValCysGlyGlySerIleLeuAspProHisTrpValLeuThrAla	TACGACAAACAGCACGTCTGTGTGTGTGTTTTTTTTTTT	AlaHisCysPheArgLysHisThrAspValPheAsnTrpLysValArgAlaGlySerAsp	GCCCACTGCTTCAGGAAACATACCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGAC	LysLeuGlySerPheProSerLeuAlaValAlaLysIleIleIleIleGluPheAsnPro	AAACTGGGCAGCTTCCCATCCCTGGCTGTGGCCAAGATCATCATCATTGAATTCAACCCC
•	s: :		SerTri	CTTG	euAsi	TGGAC	AsnTrr	VACTGC	ysile	AAGATO
	Length: Matches: Conservative Mismatches: Indels: Gaps:		AlAsp8	GGAT	rilei	CATC	1 Phe	GTTC	1Alai	
	Length: Matches Conserv Mismatc Indels: Gaps:	2063)	AspVe	TCTG	Glyse	GGGAC	AspVa	GATG	Alava	
		3 (1-	laLeu	AGGCC	'ysG13	GTGGA	isThr	ATACC	erLeu	CCCTG
	2.65e-120 1266.00 98.29% 97.44% 79.12%	S7443	yTyra	 GGAGG	sValC	CGTCT	gLysH	GAAAC	ePros	CCCAT
	2.65e-1 1266.00 98.29% 97.44% 79.12%	x AB	31yG]	 36766	GlnHi	CAGCA	PheAr	TTCAG	SerPh	AGCTT
,	ty:	.292)	leval	GGTG	spLys	ACAAA	SCys	ACTGC	euGly	- -   GGGC
	es: rity; ilari	9 (1-	Lysi	CGTGTGC	Tyra	TACG	AlaH			
	Scor : imila 1 Sim	-745-	51	804	71	864	91	924	111	984
ı	lignment Scores: red. No.: core: ercent Similarity: est Local Similarity: uery Match:	iS-09-607-745-9 (1-292) x ABS74433 (1-2063)								
	lignm red. core: ercen est L uery	iS-0	<u>≯</u>	ਰ,	≱	ā	≱	ā	≱	ā

QY Dp	131 MetTyrProLysAspAsnAspIleAlaLeuMetLysLeuGlnPheProLeuThrPheSer 150 
<u>۸</u>	151 GlyThrValArgProIleCysLeuProPhePheAspGluGluLeuThrProAlaThrPro 170
7 AG	1 LeuTrpileileGlyTrpGlyPheThrLysGlnAsnGlyGlyLysMetSerAspileLeu 190
S Y	191 LeuGinAlaSerValGinValileAspSerThrArgCysAsnAlaAspAspAlaTyrGin 210
त है ह	211 GlyGluValThrGluLysMetMetCysAlaGlyIleProGluGlyGlyValAspThrCys 230
ad yo	84 GGGGAAGICACCGAGAAGAIGAIGIGIGCAGGCAICCCGGAAGGGGGGIGIGGACACCIGC 134 31 GlnGlyAspSerGlyGlyProLeuMetTyrGlnSerAspGlnTrpHisValValGlyIle 250
90 XX	344 CAGGGTGACAGTGGTGGGCCCCTGATGTACCAATCTGACCAGTGGCATGTGGTGGGCATC 140 251 ValSerTrpGlyTyrGlyCysGlyGlyProSerThrProGlyValTyrThrLysValSer 270
8 & A	5
RES ABK ID	r 11 190 NBK11090 standard: cDNA: 2063 BP
AXX	NBK11090;
XES	05-JUN-2002 (first entry)
<b>₹</b> □ }	cDNA encoding tumour-associated antigenic target protein, TAT135.
Y K K K K K	TAT135; Tumour-associated Antigenic Target; tumour; breast cancer; colorectal cancer; lung cancer; ovarian cancer; central nervous system cancer; liver cancer; bladder cancer; melanoma; pancreatic cancer; leukaemia; gene therapy; gene; ss.
X S X	iomo sapiens.
ARTETT:	Key Location/Qualifiers CDS 2101508 /*tag= a /product= "TAT135" /note= "Tumour-associated antigenic target"
X K	10200216429-A2.
AX G	28-FEB-2002.
X G' }	2-JUN-2001; 2001WO-US20118
**************************************	24-AUG-2000; 2000WO-US23328. 26-SEP-2000; 2000US-235451P. 01-DEC-2000; 2000WO-US32678. 28-FEB-2001; 2001WO-US06520. 01-MAR-2001; 2001WO-US06666.
¥ & \$	(GETH ) GENENTECH INC.
A T T X	Goddard A, Godowski PJ, Gurney AL, Hillan KJ, Polakis P, Smith ${\rm V}_i$ Wood WI, Wu TD, Zhang Z;
DR	WPI; 2002-280917/32.

P-PSDB; AAU76535

polypeptides which are -associated antigenic target recancer therapy and diagnosis Novel isolated tumour-useful as targets for

English Claim 1; Fig 2; 121pp

The invention relates to an isolated tumour-associated antigenic target polypeptide (TAT) (1), specifically TAT134-TAT138 polypeptides, and the polypeptide (TAT) (1), specifically TAT134-TAT138 polypeptides, and the polypucidectides (II) encoding them. (II) is useful for diagnosing the presence of a tumour in a mammal, where the level of expression of (II) is indicative on the presence of tumour in the mammal from which the test sample was obtained. Antibody to (I) is useful for killing a cancer cell, a breast cancer cell, a central nervous system (CNS) cancer cell, a liver cancer cell, a bladder cancer cell, a pancreatic cancer cell, a melanoma cell or a leukaemia cell) that expresses (I). Oligonucleotides hybridising to (II) are useful as diagnostic probes, antisense hybridising to (II) is also useful in chromosome and gene mapping and in the generation of antisense RNA and DNA probes, for constructing the generation of antisense RNA and DNA probes, for constructing cancer cell in a malysis of individuals with genetic disorders. (II) is also useful for generating either transgenic animals or knockout animals, and in gene therapy. The TAT polypeptides and nucleic acids may also be used for tissue typing and the TAT polypeptides are useful for screening compounds that mimic the TAT polypeptide (agonist) or prevent the effect of TAT polypeptide from cells, for detection and quantitation of TAT polypeptide from cells, for detection and quantitation of TAT polypeptide from cells, in an enzyme linked immunosorbent assay (ELISA) or Western blot. The antibodies are also useful for treating a TAT-expressing cancer or alleviating one or more symptoms of cancer in a mammal. The present sequence represents the

576 G; 419 T; 0 other; ပ် A; 591 477 BP;

2063 228 8 0 0 0 0 0 0 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: 65e-120 66.00 3.29% 1.44% 2400 2400 4400 'ercent Similarity:
lest Local Similarity:
nery Match:
18: .lignment Scores:

ABK11090 (1-2063) × IS-09-607-745-9 (1-292)

LysilevalglyglyTyrAlaLeuAspvalAspSerTrpProTrpGlnValSerIleGln |||| |GGGGAGGAGGCCTCTGTGGATTCTTGGCCTTGGCAGGTCAGCATCCAG 804 CGTGTGGTGGG 51 ŏ ∵≿

TyrAspLysGlnHisValCysGlyGlySerlleLeuAspProHisTrpValLeuThrAla CACGTCTGTGGAGGGAGCATCCTGGACCCCCACTGGGTCCTCACGGCA TACGACAAACAG 864 71

≿ ō

02-JUN-1999; 01-SEP-1999; 15-SEP-1999; 01-DEC-1999; 02-DEC-1999;

ArgiysHisThrAspValPheAsnTrpiysValArgAlaGlySerAsp AlaHisCysPhe GCCCACTGCTTC 924 91

AspasnaspilealaLeuMetLysLeuGlnPheProLeuThrPheSer MetTyrProLys AAACTGGGCAGC 984 131

ATGTACCCCAA

1044

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130

PheProSerLeuAlaValAlaLysIleIleIleIleGluPheAsnPro

LysLeuGlySer

111

ProlleCysLeuProPhePheAspGluGluLeuThrProAlaThrPro GlyThrValArg 151 1104

LeuTrpllelleGlyTrpGlyPheThrLysGlnAsnGlyGlyLysMetSerAsplleLeu 190

171

1223 230 250 270 Human, PRO, secreted, transmembrane, cytostatic, TNF-alpha, blood, gene, tumour necrosis factor alpha release, chondrocyte cell; proliferation, differentiation; tumour, gene therapy; ss. CTCTGGATCATTGGATGGGGCTTTACGAAGCAGAATGGAGGGAAGATGTCTGACATGCTG LeuGlnAlaSerValGlnVallleAspSerThrArgCysAsnAlaAspAspAlaTyrGln ValSerTrpGlyTyrGlyCysGlyGlyProSerThrProGlyValTyrThrLysValSer CTGCAGGCGTCAGGTCATTGACAGCACACGGGTGCAATGCAGACGATGCGTACCAG GlyGluValThrGluLysMetMetCysAlaGlyIleProGluGlyGlyValAspThrCys GGGGAAGTCACCGAAAGATGATGTGTGTGCAGGCATCCCGGAAGGGGGTGTGGGACACCTGC GlnGlyAspSerGlyGlyProLeuMetTyrGlnSerAspGlnTrpHisValValGlyIle CAGGGTGACAGTGGGGCCCCTGATGTACCAATCTGACCAGTGGCATGTGGTGGGCATC GTTAGCTGGGGCTATGGCTGCGGGCCCCGAGCACCCCCAGGAGTATACACCCAAGGTCTCA 1464 GCCTATCTCAACTGGATCTACAATGTCTGGAAGGCTGAGCTG 1505 AlaTyrLeuAsnTrplleTyrAsnValTrpLysAlaGluLeu 284 ВP ACA57847 standard; cDNA; 2063 (first entry) Human PRO1570 cDNA 10-JUN-2003 ACA57847; 1404 1164 191 1224 211 1284 231 1344 251 271 RESULT 12 ACA57847 δ ద  $\delta$  $\delta$ d

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01-DEC-1999; 99WO-US21090.
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22-FEB-2000; 2000WO-US04342.
24-FEB-2000; 2000WO-US05601.
02-MAR-2000; 2000WO-US05641.
15-MAR-2000; 2000WO-US05641.
15-MAR-2000; 2000WO-US05641.
15-MAR-2000; 2000WO-US05641.
17-MAY-2000; 2000WO-US06439. 000WO-US14941 30-MAY-2000; 20 02-JUN-2000; 20 28-JUL-2000; 20 

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The invention relates to an antibody that binds to a polypeptide with a fully defined sequence given in the specification. The methods and compositions (containing antibodies that specifically bind a PRO polypeptide) of the present invention are useful for the preparation of medicament for the treatment of disorders associated with the aberrant expression or activity of the PRO polypeptide, such as tumour conditions and cancer. They can also be used to generate transgenic or knockout animals useful in the development and screening of therapeutically useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated antibody specifically binding a PRO polypeptide, useful for the preparation of a medicament for treating disorders with the aberrant expression or activity of the PRO polypeptide, such as tumor conditions and cancer
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Wood WI;
                          Human; ss; gene; gene therapy; tumour; cancer
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Watanabe CK,
                                                                                                                                                                   30-DEC-1998; 98KR-0062142.
08-MAR-1999; 99WO-US05028.
14-MAY-1999; 99WO-US10733.
30-DEC-1999; 99WO-US31274.
18-FEB-2000; 2000WO-US05601.
01-MAR-2000; 2000WO-US05601.
02-MAY-2000; 2000WO-US05601.
21-MAY-2000; 2000WO-US0564.
22-MAY-2000; 2000WO-US15264.
22-MAY-2000; 2000WO-US15264.
24-MG-2000; 2000WO-US33038.
10-NOV-2000; 2000WO-US33678.
20-DEC-2000; 2000WO-US33678.
20-DEC-2000; 2000WO-US33678.
20-DEC-2000; 2000WO-US33678.
20-DEC-2000; 2000WO-US336139.
25-AUG-1999; 99US-0330139.
25-AUG-1999; 99US-0330139.
25-AUG-1999; 99US-0330139.
25-AUG-1999; 99US-0330139.
25-AUG-1999; 99US-043344.
12-NOV-1999; 99US-0423844.
22-AUG-2000; 2000US-0664610.
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22-AUG-2000; 2000US-0644848.
18-SEP-2000; 2000US-0664610.
18-SEP-2000; 2000US-0665350.
08-NOV-2000; 2000US-0709238.
20-DEC-2000; 2000US-0747259.
22-MAR-2001; 2001US-0816744.
10-MAY-2001; 2001US-0854208.
10-MAY-2001; 2001US-0854280.
30-MAY-2001; 2001US-0874503.
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P-PSDB; ABU71561.
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        molecular weight markers for protein electrophoresis, chromosome dentification and tissue typing. The PRO polypeptides are useful to identification and tissue typing. The PRO polypeptides are useful to induce angiogenesis e.g wound healing, in the treatment of sports-related joint problems, articular cartilage defects, osteoarthritis or rheumatoid arthritis; diabetes; hyperinsulinaemia and hypoinsulinaemia. The antibodies may be used in various diagnostic, competitive binding and/or immunoprecipitation assays. The present sequence represents a cDNA encoding a PRO polypeptide of the invention.
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The invention describes novel isolated PRO polypeptides. The PRO polypeptides or anti-PRO antibodies are useful in preparing a medicament for treating a condition that is responsive to the PRO polypeptide or antibody. The PRO nucleotide sequences may be used as hybridisation probes in chromosome and gene mapping, or in generating antisense RNA and DNA. PRO nucleic acids are also useful in preparing PRO polypeptides, in assays to identify other proteins or molecules involved in binding reaction, to generate transgenic animals or knockout animals, which in turn are useful in the development and screening of therapeutically useful reagents, for chromosome identification, and tissue typing. The PRO polypeptides and nucleic acid molecules are also useful in gene therapy, and as molecular weight markers for protein electrophoresis purposes. The anti-PRO antibodies may be used in diagnostic assays for PRO, or for the affinity purification of PRO from recombinant cell culture or natural sources. This sequence encodes a novel human secreted and transmembrane PRO polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         923
                                                                                                                             chromosome mapping; gene mapping; transgenic animal; knockout animal; therapeutic agent screening; chromosome identification; tissue typing
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knockout animal;
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                                                human secreted and transmembrane protein PRO1570 cDNA.
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P-PSDB; ABU72007.
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Grimaldi JC,
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          LysHisThrAspValPheAsnTrpLysValArgAlaGlySerAsp
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gene expression; gene;
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Watanabe CK,
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         91 AlaHisCysPheArg
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                                                                                                 131 MetTyrProLysAs
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                            924 GCCCACTGCTTCAG
                                                                                                                                                                                           171 LeuTrpileileGl
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anti-PRO antibody; diag
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Grimaldi JC, Gurney AL
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   and
                                                                                           The present invention relates to the isolation of novel human PRO polypeptides, and the polynucleotide sequences encoding them. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides and polynucleotides are useful for preparing a medicament useful in the treatment of a condition responsive to anti-PRO antibody. Anti-PRO antibodies are useful in diagnostic assays for PRO, by detecting its expression in specific cells, tissues or serum, and for affinity purification of PRO from recombinant cell culture or natural sources. ACA63373-ACA63456 represent cDNA sequences encoding the human PRO polypeptides of the invention.
ide, useful for detecting and purifying the polypeptide treating conditions responsive to the antibody -
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Matches:
Conservative:
Mismatches:
Indels:
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earch completed: November 23, 2003, 08:07:00 ob time : 280.081 secs

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ALIGNMENTS

Sequence 18, Application US/09008271A

Sequence 18, Application US/09008271A

Sequence 18, Application US/09008271A

Hillman, Jennifer L.

Yue, Henry

GRNERAL INFORMATION:

Tue, Henry

Guegler, Karl J.

Corley, Neil C.

Tang, Tom Y.

Shah, Purvi

TITLE OF INVENTION: HUMAN PROTEASE MOLECULES

NUMBER OF SEQUENCES: 24

CORRESPONDENCES: 14

CORRESPONDENCES: 1

ADDRESSEE: Incyte Pharmaceutica STREET: 3174 Porter Dr.

CITY: Palo Alto

STREET: 3174 Porter Dr.

STATE: CA

COUNTRY: US?

ZIP: 9^*

NAPUTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/008,271A
FILING DATE: 16-Jan-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
FILING DATE: <Unknown>
FILING DATE: <Unknown>
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REGISTRATION NUMBER: 41,201
REFERENCE/DOCKET NUMBER: PF-0458 US
US-08-508-448C-15

US-09-370-838-79

US-09-370-838-55

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US-09-342-749-29

US-09-342-749-1

US-09-342-749-1

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US-09-691-840-29

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Matches:
Conservative:
Mismatches:
Indels:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 2038 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: COLNNOT13
CLONE: 1337018
SEQUENCE DESCRIPTION: SEQ ID NO:
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97.44%
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RESULT 2
US-09-656-002-1
i Sequence 1, Application US/09656002
i Sequence 1, Application US/09656002
i Patent No. 6455668
i GENERAL INFORMATION:
i APPLICANT: Milson, Keith
i APPLICANT: Wilson, Keith
i TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSING COLORECTAL CANCER, COMP
TITLE OF INVENTION: OF SCREENING FOR COLORECTAL CANCER MODULATORS
i TITLE OF INVENTION: OF SCREENING FOR COLORECTAL CANCER MODULATORS
i TILLE OF INVENTION: OF SCREENING FOR COLORECTAL CANCER MODULATORS
i FILE REFERENCE: A-69108/DJB/AMS
i CURRENT FILING DATE: 2000-09-06
i PRIOR FILING DATE: 2000-03-15
i PRIOR FILING DATE: 2000-01-28
i PRIOR FILING DATE: 2000-01-28
i PRIOR FILING DATE: 2000-03-15
i NUMBER OF SEQ ID NOS: 3
i SOFTWARE: Patentin version 3.0
i LENGTH: 2079
i TYPE: DNA
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APPLICANT: Andrade-Gordon, Patricia APPLICANT: Darrow, Andrew APPLICANT: Qi, Jian-shen TITLE OF INVENTION: DNA encoding the novel hur; FILE REFERENCE: ORT-1032; CURRENT APPLICATION NUMBER: US/09/386,653A; CURRENT FILING DATE: 1999-08-31; NUMBER OF SEQ ID NOS: 11; SOFTWARE: Patentin Ver. 2.0; SEQ ID NO 8; LENGTH: 1130
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ORGANISM: Artificial Sequence
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                    GlyCysGlyGlyProSerThrProGlyValTyrThrLysValSer
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Matches:
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3-09-387-375-8
Sequence 8, Application US/09387375
Patent No. 6485957
GENERAL INFORMATION:
APPLICANT: Darrow, Andrew
APPLICANT: Andrade-Gordon, Patricia
APPLICANT: Qi, Jenson
TITLE OF INVENTION: DNA Encoding the Human S
TITLE OF INVENTION: Protease BOS
FILE REFERENCE: ORT-1031
CURRENT APPLICATION NUMBER: US/09/387,375
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.0
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LENGTH: 1130
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---AsnaspilealaLeuMetLysLeuGlnPheProLeuThrPheSerGlyThrVal
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CTCATCGCGGAGCAGTGCGTCTCACGCTGCTTCCGCAACACTCTGAGACG
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S-09-386-642-7
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133 GCTCTTGCTGCCCCCTTTGATGATGATGACAAGATCGTTGGGGGGCTATGCTCTAGAGGCC
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; OTHER INFORMATION: Description of Artificial Sequence: Fusion gene
; OTHER INFORMATION: with homo sapien serine protease catalytic domain
US-09-386-642-7
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Mismatches:
Indels:
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Matches:
; Patent No. 6420157; GENERAL INFORMATION:
; APPLICANT: Darrow, Andrew, APPLICANT: Qi, Jenson; APPLICANT: Andrade-Gordon, Patricia; TITLE OF INVENTION: Zymogen Activation Syste; FILE REFERENCE: ORT-1028; CURRENT APPLICATION NUMBER: US/09/386,642; CURRENT FILING DATE: 1999-08-31; NUMBER OF SEQ ID NOS: 60; SOFTWARE: Patentin Ver. 2.0; SEQ ID NO 7
                                                                                                                                                                                                                                                             Sequence
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746.00
60.378
49.70%
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Best Local Similarity:
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Pred. No.:
                                                                                                                                                                                                                           LENGTH: 1169
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TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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                                                      GlyGlyProLeuMetTyrGlnSerAsp---GlnTrpHisValVal
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                                                                                                                                                                                                                                                                                                                         ESULT 6
S-09-386-629-2
Sequence 2, Application US/09386629
Patent No. 6426199
GENERAL INFORMATION:
APPLICANT: Darrow, Andrew L.
APPLICANT: Qi, Jenson
APPLICANT: Qi, Jenson
APPLICANT: Qi, Jenson
APPLICANT: Qi, Jenson
APPLICANT: Qi, Jenson
APPLICANT: OF INVENTION: Idenification and Character
TITLE OF INVENTION: Idenification and Character
FILE REFERENCE: ORT-1030
CURRENT APPLICATION NUMBER: US/09/386,629
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                             269 ValSerAlaTyrLeuAsnTrpIleTyr----
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domain in a
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-09-386-629-2
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LENGTH: 1166
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                                                                                                                                             100 ValPheAsnTrpLysValArgAlaGlySerAspLysLeuGlySerPheProSerLeuAla
                                                                                                                                                                           313 CCATACCTGTTCTCTGTGCTGGGGGCCTGGCAGCTGGGGAAC---CCTGGCTCTCGG
                                                                                                                                                                                                                                              ValAlaLysIleIleIle-----IleGluPheAsnProMetTyrPro---LysAspAsn
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                                                 11eleuAspProHisTrpValLeuThrAlaAlaHisCysPheArgLysHisThrAsp---
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APPLICANT: Qi, Jenson
APPLICANT: Qi, Jenson
APPLICANT: Andrade-Gordon, Patricia
TITLE OF INVENTION: Zymogen Activation System
FILE REFERENCE: ORT-1028
CURRENT APPLICATION NUMBER: US/09/386,642
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
LENGTH: 1052
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Patent No. 6420157
GENERAL INFORMATION:
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|GTGGACTGGATCCAGGAGGACGATGAAGAACAAT---TCTAGACAT
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 Description of Artificial Sequence: Fusion with homo sapien serine protease catalytic
                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                        TYPE: DNA
CORGANISM: Artificial Sequence
FEATURE:
CTHER INFORMATION: Description of Artificial Sequence: Fusion gene
COTHER INFORMATION: with homo sapien serine protease catalytic domain
US-09-386-642-9
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Matches:
Conservative:
Mismatches:
Indels:
                                                                               Sequence 9, Application US/09386642
; Patent No. 6420157
; GENERAL INFORMATION:
; APPLICANT: Darrow, Andrew
; APPLICANT: Qi, Jenson
; APPLICANT: Andrade-Gordon, Patricia
; TITLE OF INVENTION: Zymogen Activation System
; FILE REFERENCE: ORT-1028
; CURRENT APPLICATION NUMBER: US/09/386,642
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIN Ver. 2.0
; SEQ ID NO 9
; LENGTH: 1049
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                                                                                                                                                               TTCTGGAGGCCCCCTGGTGTGATGGT-----GCACTCCAG
                                                                                                                SerGlyGlyProLeuMetTyrGlnSerAspGlnTrpHisValVal
                                                                                                                                                                                                  oglyTyrGly---CysGlyGlyProSerThrProGlyValTyrThr
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                                                                580 ACTCTCAACTGTGCAGAAGTAAAATCTTTCCCCAGAAGAAGTGT----GAGGATGCT
                                                                                                 ThrGluLysMetMetCysAlaGlyIleProGluGlyGlyValAsp
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                      520 CAGAAGIGCACCGICICAGGCIGGGCACIGICACCAGICCCCGAGAGAAITITCCIGAC
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ce of human protease F in CFEK2 zymogen
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                      Sequence 59, Application US/09386642
Patent No. 6420157
Patent No. 6420157
GENBRAL INFORMATION:
APPLICANT: Darrow, Andrew
APPLICANT: Qi, Jenson
APPLICANT: Qi, Jenson
APPLICANT: Andrade-Gordon, Patricia
TITLE OF INVENTION: Zymogen Activation System
FILE REFERENCE: ORT-1028
CURRENT APPLICATION NUMBER: US/09/386,642
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 59
LENGTH: 1103
TYPE: DNA
ORGANISM: Artificial Sequence
FRANTOE:
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                                                                                                                                                      ValArgAlaGlySerAspLysLeuGlySerPheProSerLeuAlaValAlaLys---
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Patent No. 6420157

GENERAL INFORMATION:

APPLICANT: Darrow, Andrew

APPLICANT: Qi, Jenson

APPLICANT: Andrade-Gordon, Patricia

TITLE OF INVENTION: Zymogen Activation System

FILE REFERENCE: ORT-1028

CURRENT APPLICATION NUMBER: US/09/386,642

CURRENT FILING DATE: 1999-08-31

NUMBER OF SEQ ID NOS: 60

SOFTWARE: Patentin Ver. 2.0
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TYPE: DNA
ORGANISM: Artificial Sequence
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Matches:
Conservative:
Mismatches:
Indels:
US-09-386-642-60

Sequence 60, Application US/09386642

Patent No. 6420157

GENERAL INFORMATION:

APPLICANT: Darrow, Andrew,

APPLICANT: Andrade-Gordon, Patricia

TITLE OF INVENTION: Zymogen Activation System

FILE REFERENCE: ORT-1028

CURRENT APPLICATION NUMBER: US/09/386,642

CURRENT FILING DATE: 1999-08-31

NUMBER OF SEQ ID NOS: 60

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 60

LENGTH: 1037
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OTHER INFORMATION: sequence of
OTHER INFORMATION: vector
US-09-386-642-60
                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Artificial Sequence FEATURE:
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57.14%
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|GAGGCACTGAGGCTGAGGAAGCTGGCCGTGGCAAGTCAGT
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Patent No. 6444425
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Mohamath, Roadoh
APPLICANT: Mohamath, Roadoh
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Conservative:
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TYPE: DNA
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TITLE OF INVENTION: NUCLEIC ACID SEQUENCE ENCODING
TITLE OF INVENTION: TRYPSIN-LIKE ENZYME AND PROCESS FOR PRODUCING THE
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
----ACATTICCTAAACTAAGAATGAGAGTAAGAAATATTTAATTCAT
                                        127 GluPheAsnProMetTyrProLysAspAsnAspIleAlaLeuMetLysLeuGlnPhePro
                                                                                                                                                                 LeuThrPheSerGlyThrValArgProlleCysLeuProPhePheAspGluGluLeuThr
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                                                                            AACAATTATAAATCTGCAACTCATGAAAATGACATTGCACTTGTGAGACTTGAGAACAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Wenderoth, Lind & Pc
STREET: 805 Fifteenth Street, N
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
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MEDIUM TYPE: Diskette, 3.5
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/5
FILING DATE: July 28, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
781 ATTTCCACA-
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ACATTTCCTAAACTAAGAATGAGAGTAAGAAATATTTTAATTCAT
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Matches:
Conservative:
Mismatches:
Indels:
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                                                    MOLECULE TYPE: CDNA to ORIGINAL SOURCE: ORGANISM: Homo sapien TISSUE TYPE: trachea
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LENGTH: 1517 base pai
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              TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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sst Local Similarity;
                                                                                                            3-08-508-448C-15
                                                                                                                                      ignment Scores
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SSULT 14 5-09-370-838-79 Sequence 79, Application US/ Patent No. 6444425 GENERAL INFORMATION:

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891 GTCACCTTTACCAAAGATATCCATAGTGTGTGTCTCCCAGCTGCTACCCAGAATATTCCA 950
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APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Moaduh
APPLICANT: Secriet, Heather
TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGN
TITLE OF INVENTION: LUNG CANCER AND METHODS FOR THE
FILE REFERENCE: 210121.475C1
CURRENT APPLICATION NUMBER: US/09/370,838
CURRENT FILING DATE: 1999-08-09
EARLIER PPLICATION NUMBER: US 09/285,323
EARLIER FILING DATE: 1999-04-02
NUMBER OF SEQ ID NOS: 289
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 79
LENGTH: 2790
TYPE: DNA
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
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Best Local Similarity:
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891 GTCACCTTTACCAAGATATCCATAGTGTGTGTGTCCCAGCTGCTACCCAGAATATTCCA
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                                                                              SULT 15
-09-370-838-55
Sequence 55, Application US/09370838
Patent No. 6444425
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Mohamath, Roadoh
APPLICANT: Mohamath, Roadoh
APPLICANT: Mohamath, Roadoh
APPLICANT: Mohamath, Roadoh
APPLICANT: Mohamath, Roadoh
APPLICANT: Mohamath, Roadoh
APPLICANT: Mohamath, Roadoh
APPLICANT: Mohamath, Roadoh
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOUNDS FOR THERR USFILLE REFERENCE: 210121-475C1
CURRENT APPLICATION NUMBER: US/09/370,838
CURRENT FILING DATE: 1999-08-09
EARLIER APPLICATION NUMBER: US 09/285,323
EARLIER FILING DATE: 1999-04-02
NUMBER OF SEQ ID NOS: 289
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 55
LENGTH: 1462
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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265 ValfyrfhrbysvalseralafyrLe
1248 GTGTATACTCGAGTGACAGCCTACCT
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US-10-063-735-111

US-10-066-130A-274

US-10-1066-172A-124

US-10-1066-172A-124

US-10-1066-172A-274

US-10-1084-457-329

US-10-1184-642-329

US-10-1184-642-329

US-10-1184-642-329

US-10-113-689-329

US-10-173-698-329

US-10-173-698-329

US-10-173-698-329

US-10-173-698-329

US-10-173-698-329

US-10-174-583-329

US-10-174-583-329

US-10-175-746-329

US-10-175-746-329

US-10-175-746-329

US-10-175-748-329

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Guegler, Karl J.
Corley, Neil C.
Tang, Tom Y.
Shah, Purvi
TITLE OF INVENTION: HUMAN PROTEASE MOLECULES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-176-922-329
US-10-176-924-329
US-10-176-984-329
US-10-179-508-329
US-10-179-512-329
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US-10-180-719-18
Sequence 18, Application US/10180719
Publication No. US20030166246A1
GENERAL INFORMATION:
Hallman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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STREET: 3174 Porter D
CITY: Palo Alto
STATE: CA
COUNTRY: USA
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COMPUTER READABLE FORM:
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ommand line parameters:

### Applications NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1

### OOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62

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| PRANS=human40.cdi -LIST=45 -DOCALIGN=20 -THR SCORE=pct -THR MAX=100

| PRANS=human40.cdi -LIST=45 -DOCALIGN=20 -THR SCORE=pct -THR MAX=100

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| PRANS=human40.cdi -LIST=45 -DOCALIGN=20 -THR MAX=100

| PRANS=NAMA - LIST=45 -DOCALIGN=20 -MAIT -DSPBLOCK=100

| PRANS=NAMA - LARGEQUERY - NEG SCORE=pc - MAIT -DSPBLOCK=100

| PRANS=NAMA - LARGEQUERY - NEG SCORE=pc - MAIT - NEGAPEXT=0.5

| PRANS=NAMA - LARGEQUERY - NEGAPEXT=0.5 -DELOP=6 -DELEXT=7

| PRANS=NAMA - LARGEQUERY - NEGAPEXT=0.5 -DELOP=6 -DELEXT=7
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                                                                                                           2003, 07:54:55; Search time 314.091 Seconds (without alignments) 3038.343 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBGOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
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11: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
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               GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd.
                                                                                 frame_plus_p2n model
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CORGANISM: Homo Sapien
US-09-888-257A-2
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Best Local Similarity:
Query Match:
DB:
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
        CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/180,719
FILING DATE: 25-Jun-2002
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/008,271
FILING DATE: 16-Jan-1998
ATTORNEY/AGENT INFORMATION:
NAME: Mohan-Peterson, Sheela
REGISTRATION NUMBER: 41,201
REFERENCE/DOCKET NUMBER: PF-0458 US
TELEPHONE: 650-855-0555
TELEPHONE: 650-845-4166
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 2038 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LERRANCE: COLNNOT13
EQ for Windows Version
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SEQUENCE DESCRIPTION
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                            ValSerTrpGlyTyrGlyCysGlyGlyProSerThrProGlyValTyrThrLysValSer
            271 AlaTyrLeuAsnTrpIleTyrAsnValTrpLysAlaGluLeu 284
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us-09-607-745-9.rnpb

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Transmembrane Polypeptides and Nucleic
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CURRENT APPLICATION NUMBER: 60/09946,374
CURRENT FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/099735
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Williams, P. Mickey
Wood, William I.
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Sequence 274, Application US/09946374
Publication No. US20030073129A1
GENERAL INFORMATION:
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APPLICANT: Botstein, David
APPLICANT: Botstein, David
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christophe:
APPLICANT: Grimaldi, Christophe:
APPLICANT: Hillan, Kenneth J.
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Paoni, Nicholas
Roy, Margaret An
Smith, Victoria
Stewart, Timothy
Tumas, Daniel
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PRIOR APPLIC PRIOR PLING PRIOR PILING PRIOR PILING	Alignment Scores: Pred. No.; Score: Percent Similarit Best Local Simila Query Match: DB:	US-09-607-745-9	Oy 51 Ly Db 804 CC	Oy 71 T) Db 864 T	Oy 91 Al Db 924 GC	Oy . 111 Ly Db 984 AZ	Oy 131 Me     Db 1044 A1	Oy 151 G1         Db 1104 GC	Oy 171 Le	Qy 191 Le
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; ORGANISM: Homo Sapien
US-10-063-735-111
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Pred. No.:
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                                                                                                            GGGCCCCTGATGTACCAATCTGACCAGTGGCATGTGGTGGGCATC
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Encoding the Same
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Matches:
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- See File Wrapper
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-12-12
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Sequence 274, Application US/10015387A
Publication No. US20030135034A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Botstein, David
APPLICANT: Forny, Sherman
APPLICANT: Ferrara, Napoleone
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gao, Wei-Qiang
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Grimaldi, Secreted and Transm.
TITLE OF INVENTION: Secreted and Transm.
TITLE OF INVENTION: Acids Encoding the
FILE REFERENCE: P2830PIC54
CURRENT APPLICATION NUMBER: US/10/015,3
CURRENT FILING DATE: 2001-12-12
Prior Application removed - See File Wr
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US-10-063-735-111
Sequence 111, Application US/10063735
Fublication No. US20030138802A1
GENERAL INFORMATION:
APPLICANT: Eaton, Dan L.
APPLICANT: Garintsen, Mary E.
APPLICANT: Goddard, Audrey,
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Grimaldi, Christopher J.
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APPLICANT: Wacanabe, Colin K.
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APPLICANT: Waca
984 AAACTGGGCAGCTTCCCATCCCTGGCTGTGGCCAAGATCATCATCATTGAATTCAACCCC
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Conservative:
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; NUMBER OF SEQ ID
; SEQ ID NO 274
; LENGTH: 2063
; TYPE: DNA
; ORGANISM: HOMO S
US-10-006-130A-274
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APPLICANT: Baker, Kevin F.
APPLICANT: Betsein, David
APPLICANT: Eaton, Dan 1.
APPLICANT: Eaton, Dan 1.
APPLICANT: Ferrara, Napoleone
APPLICANT: Gao, Wel-Olang
APPLICANT: Gao, Wel-Olang
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Pan, James
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2830PLC7
CURRENT APPLICATION NUMBER: US/10/006,130A
CURRENT FILING DATE: 2002-03-19
Prior Application removed - See File Wrapper or Palm
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                                                                       LysHisThrAspValPheAsnTrpLysValArgAlaGlySerAsp
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                                                       TyrasplysGlnHisValCysGlyGlySerIleLeuAspProHisTrpValLeuThrAla
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Sequence 274, Application US/10006130A
Publication No. US20030148375A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eaker, Kevin P.
Baker, Kevin P.
Beststein, David
Beststein, David
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Beststein, David
Beststein, David
Gao, Wei-Qiang
Goddard, Audrey
Godowski, Paul J.
Grimaldi, Christopher J.
Hillan, Kenneth J.
Pan, James
Beoni, Nicholas F.
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Mismatches:
Indels:
Gaps:
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Matches:
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US-10-199-672-329
; Sequence 329, Application US/10199672
; Publication No. US20030148442A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
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Query Match:
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APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRY
TITLE OF INVENTION: ACIDS ENCODING THE SAMM
FILE REFERENCE: P3430R1C1
CURRENT APPLICATION NUMBER: US/10/199,672
CURRENT FILING DATE: 2002-01-15
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/063250
PRIOR APPLICATION NUMBER: 60/063120
PRIOR FILING DATE: 1997-10-17
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PRIOR PILING DATE: 1998-09-29
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PRIOR FILING DATE: 1998-10-26
PRIOR APPLICATION NUMBER: 60/105807
PRIOR FILING DATE: 1998-10-27
PRIOR APPLICATION NUMBER: 60/105881
PRIOR FILING DATE: 1998-10-27
PRIOR APPLICATION NUMBER: 60/105882
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Sequence 329, Application US/10187749
Publication No. US20030153036A1
GENERAL INFORMATION:
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Matches:
Conservative:
Mismatches:
Indels:
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98.29%
97.44%
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; ORGANISM: Homo Sapien
US-10-187-749-329
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Best Local Similarity:
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Alignment Scores Pred. No.:
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APPLICANT: Goddard, Austin L.
APPLICANT: Gurney, Austin L.
APPLICANT: Gurney, Austin L.
APPLICANT: Mith, Victoria
APPLICANT: Mainth, Victoria
APPLICANT: Mith, Victoria
APPLICANT: Mainth, Victoria
APPLICANT: Mainth, Victoria
APPLICANT: Mainth, Victoria
APPLICANT: Mainth, Victoria
APPLICANT: Mainth, Victoria
APPLICANT: ACIDS ENCODING THE SAME
TITLE OF INVENTION: SERETETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SERETETE AND TRANSMEMBRANE POLYPEPTIDES
CURRENT FILING DATE: 1002-01-11
PRIOR PELICATION NUMBER: 10/52566
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/62250
PRIOR APPLICATION NUMBER: 60/62326
PRIOR PLING DATE: 1997-10-24
PRIOR PELING DATE: 1997-10-24
PRIOR PELING DATE: 1997-10-24
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GlnValIleAspSerThrArgCysAsnAlaAspAspAlaTyrGln
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Publication No. US20030153037A1
GENERAL INFORMATION:
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                         GGCACAGTCAGGCC
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Matches:
Conservative:
Mismatches:
Indels:
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US-10-184-642-329
; Sequence 329, Application US/10184642
; Publication No. US20030157635A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
                                                                                       1.6e-152
1266.00
98.29%
97.44%
79.12%
; LENGTH: 2063
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-194-457-329
                                                                                                   Score:
Percent Similarity:
Best Local Similarity;
Query Match:
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APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C194
CURRENT APPLICATION NUMBER: US/10/184,642
CURRENT APPLICATION NUMBER: US/10/184,642
CURRENT APPLICATION TEMOVED - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 329
LENGTH: 2063
TYPE: DNA
ORGANISM: Homo Sapien
S-10-184-642-329
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Gurney, Austin
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US-LILYBOY-7-329,
Sequence 329, Application US/10196747
Fublication No. US20033062250A1
Fublication No. US20033062250A1
Fublication No. US20033062250A1
Fublication No. US20033062250A1
Fublication No. US20033062250A1
Fublication Chen, Jian
APPLICANT: Chen, Jian
APPLICANT: Goddward, Audrey
APPLICANT: Goddward, Audrey
APPLICANT: Goddward, Audrey
APPLICANT: Matanabe, Colin K.
APPLICANT: Matanabe, Colin K.
APPLICANT: Matanabe, Colin K.
APPLICANT: Watanabe, 
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APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David APPLICANT: Eaton, Dan 1.
APPLICANT: Ferrara, Napoleone APPLICANT: Fong, Sherman APPLICANT: Gao, Wei-Qiang APPLICANT: Godowski, Paul J.
APPLICANT: Gotowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
      98.29%
97.44%
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APPLICANT: Baker, Kevin P.
APPLICANT: Baker, Kevin P.
APPLICANT: Baker, Kevin P.
APPLICANT: Baton, Dan 1.
APPLICANT: Eaton, Dan 1.
APPLICANT: Ferrara, Napoleone
APPLICANT: Forg, Sherman
APPLICANT: Forg, Wei-Qiang
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Gurney, Austin L.
APPLICANT: Gurney, Austin L.
APPLICANT: Gurney, Austin L.
APPLICANT: Gurney, Austin L.
APPLICANT: Gurney, Austin L.
APPLICANT: Gurney, Austin L.
APPLICANT: Fan, James
APPLICANT: Fan, James
CURRENT: Paun, James
TITLE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION NUMBER: 60/098749
FRIOR APPLICATION NUMBER: 60/098749
FRIOR PILING DATE: 1998-09-01
PRIOR PILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/098821
PRIOR APPLICATION NUMBER: 60/098821
PRIOR APPLICATION NUMBER: 60/098821
PRIOR APPLICATION NUMBER: 60/098831
PRIOR APPLICATION NUMBER: 60/098831
PRIOR APPLICATION NUMBER: 60/09856
PRIOR APPLICATION NUMBER: 60/099596
PRIOR APPLICATION NUMBER: 60/099596
PRIOR PRING DATE: 1998-09-09
PRIOR PILING DATE: 1998-09-09
PRIOR PILING DATE: 1998-09-09
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Sequence 274, Applica
Publication No. US200
GENERAL INFORMATION:
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NUMBER OF SEQ ID
SEQ ID NO 274
LENGTH: 2063
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DNA ORGANISM:

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LysLeuGlySerPheProSerLeuAlaValAlaLysIleIleIleIleGluPheAsnPro 130
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; Sequence 329, Application US/10173689
; Publication No. US20030166104A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Chen,Jian
; APPLICANT: Goddard,Audrey
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Smith,Victoria
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Shang,Zemin I.
; APPLICANT: Watanabe,Colin K.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCL.
; TITLE OF INVENTION: SCRETED AND TRANSMEMBRANE POLYPEPTIDES
; TITLE OF INVENTION: SCRETED AND TRANSMEMBRANE
; TITLE OF INVENTION: SCRETED AND TRANSMEMBRANE
; TITLE OF SEQ ID NOS: 612
; SEQ ID NOS: 612
; SEQ ID NOS: 612
; LENGTH: 2063
; TUPE: NAN
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Conservative:
Mismatches:
Indels:
Gaps:
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APPLICANT: Paoni, Nicholas F.

TITLE OF INVENTION: Secreted and Transmembra
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P283 OP1C62
CURRENT APPLICATION NUMBER: US/10/017,253A
CURRENT FILING DATE: 2001-12-13
PRIOR FILING DATE: 1998-09-01
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X	131 MetTyr	MetTyrProLysAspAspAspIleAlaLeuMetLysLeuGlnPheProLeuThrPheSer 150
д	1044 ATGTAC	ATGTACCCCAAAGACAATGACATCGCCCTCATGAAGCTGCAGTTCCCACTCACT
X	151 GlyThr	GlyThrValArgProIleCysLeuProPhePheAspGluGluLeuThrProAlaThrPro 170
д	1104 GGCACA	GGCACAGTCAGCCCATCTGTCTTTTTTTTTTTTTTTTTT
X	171 LeuTrp	LeuTrpileileGlyTrpGlyPheThrLysGlnAsnGlyGlyLysMetSerAspileLeu 190
д	1164 CTCTGG	CTCTGGATCATTGGATGGGGCTTTACGAAGCAGAAGGGAAGATGTCTGACATACTG 1223
<b>&gt;</b>	191 LeuGln	LeuGlnAlaSerValGlnValIleAspSerThrArgCysAsnAlaAspAspAlaTyrGln 210
д	1224 CTGCAG	CTGCAGGCGTCAGTCCAGGTCATTGACACGCACACGGTGCAATGCAGACGATGCGTACCAG 1283
γ	211 GlyGlu	GlyGluValThrGluLysMetMetCysAlaGlylleProGluGlyGlyValAspThrCys 230
д	1284 GGGGAA	GGGGAAGTCACCGAGAAGATGATGTGTGCAGGCATCCCGGAAGGGGGGTGTGGACCTGC 1343
λ	231 GlnGly	GlnGlyAspSerGlyGlyProLeuMetTyrGlnSerAspGlnTrpHisValValGly1le 250
д	1344 CAGGGT	CAGGGTGACAGTGGGCCCCTGATGTACCAATCTGACCAGTGGCATGTGGGGGCATC 1403
>	251 ValSer	ValSerTrpGlyTyrGlyCysGlyGlyProSerThrProGlyValTyrThrLysValSer 270
ą	1404 GTTAGO	GTTAGCTGGGGCTATGGCTGCGGGGCCCCGAGCACCCCAGGAGTATACACCAAGGTCTCA 1463
×	271 AlaTyr	AlaTyrLeuAsnTrpIleTyrAsnValTrpLysAlaGluLeu 284
,Ω	1464 GCCTAT	GCCTATCTCAACTGGATCTACAATGTCTGGAAGGCTGAGCTG 1505

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NITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45

NOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL

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USER=US09607745_@CGN 1_1_3596_@runat_21112003_144346_22229 -NCFU=6 -ICFU=3

NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG

NEW TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6

PGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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## 9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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RGANISM Homo sapiens (human)
RGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMM10409 row: e column: 23
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Analysis of the.mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.

Adalysis of the.mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.

Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hiranoto,K., Hiraoka,T., Hiraoka,T., Harozane,T., Hayashida,K., Tayatus,N., Haranoto,K., Haraka,T., Kasukawa,T., Kasukawa,T., Kasukawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kawai,M., Okazaki,R., Nomura,K., Numazaki,R., Ohno,M., Ohsac,S., Kurihara,C., Saito,H., Saito,H., Saito,H., Saito,H., Saito,H., Saito,H., Shinagawa,A., Shiraki,T., Sadazume,N., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-722 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:Genome-res@gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9222, Fax:81-45-503-9226, Fax:81-45-503-9226, Fax:81-45-503-9226, Fax:81-45-503-9226, Fax:81-45-503-9226, Fax:81-45-503-9226, Fax:81-45-503-9226, Fax:81-45-503-9226, Fax:81-45-503-9226, Fax:81-45-503-9226, Fax:81-45-503-9226, Fax:81-45-503-9226, Fax:81-45-503-9226, Fax:81-45-503-9226, Fax:81-45-503-9226, Fax:81-45-503-9226, Fax:81-45-503-9226, Fax:81-45-503-9226, Fax:81-45-503-9226, Fax:81-45-503-9226, Fax:81-45-503-9226, Fax:81-45-503-9226, Fax:81-45-503-9226, Fax:81-45-503-9226, Fax:81-45-503-9226, Fax:81-45-503-9266, Fax:81-45-503-9266, Fax:81-45-503-9266, Fax:8
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Please visit our web site for further details.

URL:http://genome.gsc.riken.go.jp/.
URL:http://fantom.gsc.riken.go.jp/.
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\04 - 1=2-
Wang, K.H., Weitz, C., Whittaker, C., Wilming, L., 3, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S.
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                      Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsu and Hayashizaki, Y.
Functional annotation of a full-length mouse cDNA collection Nature 409 (6821), 685-690 (2001)
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/note="SIMILAR TO TRANSMEMBRANE PROTEASE,
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/db_xref="taxon:10090"

/clone="9030622G02"
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                                                                  803 CGTGTGGTGGGTGGGGTGGAGGCCCCTGTGGATTCTTGGCCGTGGCAGGTCAGCATCAG
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
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AGENCOURT 10158166 NCI CGAP CO24 Mus musculus cDNA clone IMAGE:6529422 5', mRNA sequence.
BU522841
BU522841.1 GI:22833279
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                                 LysileyalglyglyffyrAlaLeuAspvalAspSerTrpProffrgGlnVal
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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US-09-607-745-9 (1-292) x AK078890 (1-2177)
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us-09-607-745-9

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US-09-607-745-9 (1-292)
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Tissue Procurement: The Cepko Laboratory

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://inage.llnl.gov

Plate: LLAM14129 row: i column: 06

High quality sequence stop: 665.

Location/Qualifiers

Location/Qualifiers

I. 895

Organism="Mus musculus"

| mol_type="mRNA"
| well-wref="mRNA"
| well-wref="taxon:10090"
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167 CGTGTGGTGGGTGGC
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BC004855
Homo sapiens, Similar to transmembrane protease, serine 4, clone IMAGE:3835263, mRNA.
BC004855
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8347148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1973)
Strausberg, R.
Direct Submission
Submitted (21-MAR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ford, Julia
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 834714: This clone has the following problem: frame shifted.

Location/Qualifiers
1. .1973
CAGGGTGACAGTGGGCCCTTTGATGTACCATTCTGACAAGTGGCAGGTAGTAGGCATC
                                           51 LysileyalglyglyTyrAlaLeuAspValAspSerTrpProTrpGlnValSerileGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Greene, Mark Ketteman and Anuradha Madan
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/wol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3835263"
/tissue_type="Ovary, adenocarcinoma"
/clone_lib="NIH MGC 9"
/lab_host="DH10B-R"
/note="Vector: pOTB7"
a 573 c 531 g 398 t
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76.60%
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Homo sapiens
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source   1689   /organism="Mus musculus"   /mol_type="mRNA"   /mol_type="mRNA"   /strain="FVB/N"   /db_xref="taxon:10090"   /clone="IMAGE:4989048"   /lab_host="DH10B (T1 phage-resistant)"   /clone   lib="NCI CGAP Co24"   /note="Organ: colon; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.6 kb. Constructed by Life	Alignment Scores: Pred. No.: Score: Score: Ratches: Ratches: Recent Similarity: Recent Similarity: Recent Similarity: Recent Similarity: Recent Similarity: Recent Similarity: Recent Similarity: Recent Similarity: Recent Similarity: Recent Similarity: Recent Similarity: Recent Similarity: Recent Similarity: Recent Similarity: Recent Similarity: Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent Recent	Oy 75 HisValCysGlyGlySerIleLeuAspProHisTrpValLeuThrAlaAlaHisCysPhe 94	62 115 122	Oy 135 AspAsnAspIleAlaLeuMetLysLeuGlnPheProLeuThrPheSerGlyThrValArg 154 :::	175 GlyTrpGlyPheThrLysGlnAsnGlyGlyLysMetSerAspIleL6	QY         215 GluLysMetMetCysAlaGlyIleProGluGlyGlyValAspThrCysGlnGlyAspSer         234           :::   :::		RESULT 6 CB142902 LOCUS CB142902 DEFINITION K-EST0196799 L11SNU354s1 Homo sapiens cDNA clone L11SNU354s1-20-D07
71 TyrAspLysGlnHisValCysGlyGlySerIleLeuAspProHisTrpValLeuThrAla 90   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INTERPORTED   INT	1086 ATGTACCCCAAAGACAATGACATCGCCCTCATGAAGCTGCAGTTCCCACTTTCTCA 1145 151 GlyThrValArgProlleCysLeuProPhePheAspGluGluLeuThrProAlaThrPro 170 1146 GGCACAGTCAGGCCCATCTGTCTGTCTTTTGATGAGGAGCTCACTCCAGCCCCCA 1205 171 LeuTrplleIleGlyTrpGlyPheThrLysGlnAsnGlyGlyLysMetSerAspIleLeu 190 1206 CTCTGGATCATTGGATGGGGCTTTACGAAATGGA	<ul><li>191 LeuGlnAlaSerValGlnValIleAspSerThrArgCysAsnA</li><li>244</li></ul>		250 eValSerTrpGlyTyrGlyCysGlyGlyProSerThrProGlyValTyrThrLysValSe 270	5 1 BG966811 ION 602834306F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4989048 5', mRNA sequence. ON BG966811 BG966811. GI:14354448 S EST.	Mus musculus (house mouse)  ISM Mus musculus  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  CE 1 (bases 1 to 689)  RS NIH-MGC http://mgc.nci.nih.gov/.  National Institutes of Health, Mammalian Gene Collection (MGC)  AL Unpublished	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Jeffrey E. Green, M.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:	nctp://lumge.llff.gov Plate: LLAM11002 row: k column: 01 High quality sequence stop: 680. S Location/Qualifiers

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Contact: Soares, MB
Condinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
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Homo sapiens (human)
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 569)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 265 ValTyrThrLysValSerAlaTyrLeuAsnTrpileTyrAsnValTrpLysAlaGluLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   185 LysMetSerAspileLeuLeuGlnAlaSerValGlnValIleAspSerThrArgCysAsn
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Seg primer: M13 Reverse.
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/db xref="taxon:9606"
/clone="UI-E-CRO-adk-g-09-0-UI"
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/dev_stage="adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
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UI-E-CRO is a cDNA library containing the following
tissue(s): eye anterior segment. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AATGCCGCAT. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 659)

8 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

In (Dpublished Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D.,
Email: cgapbs-r@mailon: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at:

www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1830 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 450.

Incation/Qualifiers

Incation/Qualifiers
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/dev stage="adult"
/lab_host="DH10B (phage-resistant)"
/clone lib="NCI CGAP_Lu19"
/clone lib="NCI CGAP_Lu19"
/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; lst strand cDNA was prepared from pooled lung tumor tissue, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo. "

Ratima Bonaldo. "
176 c 178 g 157 t
A1924527 659 bp mRNA linear EST 08-MAR-2000 wn61c07.x1 NCI CGAP Lu19 Homo sapiens cDNA clone IMAGE:2449932 3' similar to TR:060235 060235 AIRWAY TRYPSIN-LIKE PROTEASE. ;, mRNA
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differentiated (4 pooled tumors, including primary
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NCI_CGAP_Lu19"
/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from pooled lung tumor tissue, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                            648 bp mRNA linear EST 02-SEP-1999 NCI CGAP Lu19 Homo sapiens cDNA clone IMAGE:2449197 3' TR:Ō60235 O60235 AIRWAY TRYPSIN-LIKE PROTEASE. ;, mRNA
BAAGCAGAAIGGAAGAIGICTGACAIACIGCIGCAGGCGICA 480
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                                                                        ProSerThrProGlyValTyrThrLysValSerAlaTyrLeuAsn
                                                            SAlaGlyIleProGluGlyGlyValAspThrCysGlnGlyAspSer
                                                                                                   TyrGlnSerAspGlnTrpHisValValGlyIleValSerTrpGly
                                                                                                               CCGAGCACCCCAGGAGTATACACCAAGGTCTCAGCCTATCTCAAC
                     SerThrArgCysAsnAlaAspAspAlaTyrGlnGl
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AI924182.1 GI:566
EST.
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                                                                                                    GlyGlyProLeuMet
GGATGGGGCTTTAC
                                 ValGlnValIleAs
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SFERENCE AUTHORS TITLE

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MMENT

SATURES

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BM773306

K-EST0057738 S3SNU16s1 Homo sapiens CDNA clone S3SNU16s1-17-C08 5', mRNA sequence.

NEWNA sequence.

MRNA sequence.

MRNA sequence.

MRNA3306.

BM773306.

BM773306.

BM773306.

GI:19102921

SST.

Homo sapiens (human)

ISM Homo sapiens (human)

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ISM Homo sapiens (human)

ISM Homo sapiens (human)

ISM Homo sapiens (human)

ISM Han, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Kim, M.X., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.

I (hases 1 to 563)

IN S. Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Kim, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.

I (hap, J.S. Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Contact: Kim YS

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Site_2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Topl0F' by electroporation method.
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                                                                                                                                                 206 AspAspAlaTyrGlnGlyGluValThrGluLysMetMetCysAlaGlyIleProGluGly 225
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Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
186 MetSerAspIleLeuLeuGlnAlaSerValGlnValIleAspSerThrArgCysAsnAla 205
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Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 19 row: D column: 01
High quality sequence stop: 572.
Location/Qualifiers
1. .572
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Genome Research Center
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BM747250
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MRNA sequence.
BM747250
BM747250.1 GI:19076856
SST.
Homo sapiens (human)
SM Homo sapiens
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SI (bases 1 to 578)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
21C Frontier Korean EST Project 2001
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                                                                                 Korea Research Court.

Korea Research Institute of Bioscience & Biot 52 Eceun-dong Yuscong-gu, Daejeon 305-333, So Tel: +82-42-860-4470

Fax: +82-42-860-4409

Email: yongsung@mail.kribb.re.kr

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Location/Qualifiers
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Ext. +62-46-860-4409

Email: Yongsungsunglamil. Kribb. re. kr
Plate: 22 row: C column: 01

Fax: +62-42-860-4409

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Plate: 22 row: C column: 01

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BM788163
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1 (bases 1 to 614)

Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.

21C Frontier Korean EST Project 2001

Unpublished
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Genome Research Center
Korea Research Institute of Bioscience & Bi
52 Eoeun-dong Yuseong-gu, Daejeon 305-333,
Tel: +82-42-860-4470
Fax: +82-42-860-4409
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BM772743 (1-596)

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09-607-745-9

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

			•			SUMMARIES	
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1	<u> </u>	2342		1305	1 (4)	AAD02556	seripanci
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The present invention relates to seripancrin polynucleotides, and polypeptides encoded by them. Seripancrin are members of serine protease family. This protein contains a transmembrane domain, a low density lipoprotein (LDL) domain, protease domain and a scavenger receptor cysteine-rich (SRCR) domain. The LDL and SRCR domains help to define the specificity of seripancrin's intra and intermolecular interactions. The polynucleotides and polypeptides of the invention are useful for treating and diagnosing diseases such as arthritis, chronic obstructive pulmonary disorder (COPD), cancer, osteoporosis, aberrant wound healing, angiogenesis, inflammatory disorders, diabetes, stroke and cardiovascular diseases. Seripancrin genes are useful in chromosome localisation studies, as tools for tissue expression studies and also in gene therapy. The polypeptides of the invention are used for identifying agonists and antagonists useful for treating conditions associated with seripancrin imbalance. These polypeptides are also useful as vaccines. The present sequence is a cDNA coding for seripancrin The seripancrin gene is located on human chromosome 11q22-q23.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    New extracellular serine protease Seripancrin, useful for treating cancer, osteoporosis, arthritis, chronic obstructive pulmonary disease, diabetes, inflammatory disorders, stroke, angiogenesis and aberrant wound healing -
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1261 TCAGCCTATCTCAACTGGATCTACAATGTCTGGAAGGCTGAGCTG 1305
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ESULT 2

2038 BP AAX87154 standard; cDNA

AAX87154;

(first entry) 27-SEP-1999

Human protease HUPM-6 cDNA.

HUPM-6; cell proliferation; cancer; Serine protease; human; HUFM-6; cell prolifimmune disorder; inflammation; therapy; ss.

Homo sapiens

Location/Qualifiers 200..1507 /\*tag= a Key

WO9936550-A2

22-JUL-1999.

99WO-US00655. 12-JAN-1999;

98US-0008271. 16-JAN-1998;

(INCY-) INCYTE PHARM INC

Guegler KJ, Hillman JL, Shah P; Bandman O, Corley NC, Tang YT, Yue H;

WPI; 1999-430616/36. P-PSDB; AAY06437.

Novel human protease molecules useful in the treatment of developmental disorders and/or cancers

Claim 8; Page 86-87; 90pp; English.

This nucleotide sequence codes for HUPPM-6 (see AAY06437), a novel human protease. HUPPM-6 cDNA was initially identified in Incyte Clone 1337018 from the colon cDNA library COLNNOT13 using a computer search for amino acid sequence alignments. The present sequence is a consensus sequence derived from overlapping and/or extended nucleic acid sequences: Incyte Clones 1271725 (TRSTTUT02), 1337018, 586982 and 588598 (UTRSNOT01). A fragment comprising nucleotides 900-949 of the present sequence can be used for hybridisation. This sequence encompasses an active site residue. Northern analysis shows expression of HUPPM-6 in gastrointesinal, and male an female reproductive CDNA libraries. Approximately 65% of these libraries are associated with neoplastic disorders, and 22% with the immune response. The invention provides 12 new human protectides encoding them (see AAX06432-43), and the polynucleotides encoding them (see AAX06432-43), and the polynucleotides encoding them (see AAX06432-43), and the vectors, host cells and methods for producing HUPM polypeptides, as well as agonists and antagonists of HUPM. Methods for treating or preventing cell proliferative disorders and immune disorders using HUPM or HUPM antagonists are claimed.

Sequence 2038 BP; 462 A; 591 C; 569 G; 416 T; 0 other;

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<pre>ignment Scores: ed. No.:   ore:   rcent Similarity:   st Local Similarity:   ery Match: :</pre>	2.72e-209 2338.00 100.00% 99.77% 99.83%	Length: Matches: Conservative Mismatches: Indels: Gaps:

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Db	SATCCTGACAGGATCTCTGAACAGCCTCGATGTCAAACCCCTGCGCAAACC
δy	lleProMetGluThrPheArgLysValGlyIleProlleIleIleAlaLeuLeuSer 4
gg	260 CGTATCCCCATGGAGACCTTCAGAAAGGTGGGGGATCCCCCATCATCATGACACTACTGAGC 319
٥٧	41 LeuAlaSerIleIleIleValValValLeuIleLySValileLeuAspLySTyrTyrPhe 60
ДQ	320 CIGGCGAGIAICAITGIGIIIIIIIIIIIIIIIIIIIIII
δ <sub>γ</sub>	61 LeuCysGlyGlnProLeuHisPhelleProArgLysGlnLeuCysAspGlyGluLeuAsp 80
qq	380 CICTGCGGGCACCTCTCACTTCATCCCGAGGAAGCAGCTGTGTGACGGAGAGCTGGAC 439
δλ	81 CysProLeuGlyGluAspGluGluHisCysValLysSerPheProGluGlyProAlaVal 100
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ΩÇ	500 GCAGTCCGCCTCTCCAAGGACCGATCCACACTGCAGGTGCTGGACTCGGCCACAGGGAAC 559
٥x	121 TrpPheSerAlaCysPheAspAsnPheThrGluAlaLeuAlaGluThrAlaCysArgGln 140
qq	560 regriciciecterraceacaacricacaaaaecrocecreacaeecrereraeecae
ζ	1 MetGlyTyrSerSerLysProThrPheArgAlaValGluIleGlyProAspGlnAspLeu
QQ	620 Ardederacadedaaaceeaerrreadagerereredaaarregeeeeagaeeagarere 679
Qy	161 AspValValGluIleThrGluAsnSerGlnGluLeuArgMetArgAsnSerSerGlyPro 180
qq	680 GATGITGITGAAATCACAGAAAACAGCCAGGAGCTICGCATGCGGAACTCAAGTGGGGCCC 739
٥y	181 CysLeuSerGlySerLeuValSerLeuHisCysLeuAlaCysGlyLysSerLeuLysThr 200
Ωp	740 TGTCTCTCAGGCTCCCTGGTCTCCCTGCACTGTCTTGCCTGGGGGAGGCCTGAAGACC 799
Qy	201 ProArgValValGlyGlyGluGluAlaSerValAspSerTrpProTrpGlnValSerIle 220
qq	800 CCCCGTGTGTGGGGGGGGGGGGCCTCTGTGGGTTCTTGGCCTTGGCAGGTCAGCATC 859
δy	221 GlnTyrAspLysGlnHisValCysGlyGlySerIleLeuAspProHisTrpValLeuThr 240
Ωp	860 CAGTACGACAAACAGCACGTCTGTGTGTGTTTTTTTTTT
Qy	241 AlaAlaHisCysPheArgLysHisThrAspValPheAsnTrpLysValArgAlaGlySer 260
Db	920 GCAGCCCACTGCTTCAGGAAACATACCGATGTTCAACTGGAAGGTGCGGGCAGGCTCA 979
δλ	261 AspLysLeuGlySerPheProSerLeuAlaValAlaLysIleIleIleIleGluPheAsn 280
Db	
Qy	281 ProMetTyrProLysAspAspAspAleAlaLeuMetLysLeuGlnPheProLeuThrPhe 300
gp	1040 CCCATGTACCCCAAAGACAATGACATCGCCCTCATGAAGCTGCAGTTCCCACTCACT
Qy .	301 SerGlyThrValArgProlleCysLeuProPhePheAspGluGluLeuThrProAlaThr 320
Д	00 TCAGGCACAGTCAGGCCCATCTGCTCTTTTTTTTTTTTT
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Db	60 CCACTCTGGATCATTGGATGGGCTTTACGAAGCAGAATGGAGGGAAGATGTCTGACATA 1
δ	
Ωp	20 CIGCIGCAGGCGICAGGICCAGGICAITGACAGCACAGGIGCAAIGCAGACGAIGCGIAC 12

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     CTATGGCTGCGGGGCCCGAGCACCCCCAGGAGTATACACCCAAGGTC
GluLysMetMetCysAlaGlyIleProGluGlyGlyValAspThr
                    TyrGlyCysGlyGlyProSerThrProGlyValTyrThrLysVal
                                                                   CTGGATCTACAATGTCTGGAAGGCTGAGCTG 1504
                                                             SerAlaTyrLeuAsnTrpIleTyrAsnValTrpLysAlaGluLeu
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                                                                                      BX76354
D ABX
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Lung cancer-associated polynucleotide, gene; ds; cytostatic; emphysema; antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis; small cell lung cancer; benign lesion; precancerous lesion; bronchitis; chronic obstructive pulmonary disease; hypersensitivity pneumonitis; interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.

Unidentified.

WO200286443-A2

31-OCT-2002

18-APR-2002; 2002WO-US12476.

770P. 492P. 245P. 666P. 370P. 2001US-28477 2001US-29049 2001US-33924 2001US-35066 2001US-33437 2002US-37224 18-APR-2001; 10-MAY-2001; 09-NOV-2001; 13-NOV-2001; 29-NOV-2001; 12-APR-2002; HNC (EOSB-) EOS BIOTECHNOLOGY

Murray R; Aziz N,

WPI; 2003-093161/08 P-PSDB; ABU56625.

verecting a lung cancer-associated transcript in a cell from a patient for treating lung cancer, by contacting a biological sample from the patient with a polynucleotide that exhibits increased or decreased expression in lung cancer -

Claim 22; Page 353; 453pp; English

The invention relates to a method for detecting a lung cancer-associated transcript in a cell from a patient, comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridises to a sequence that is at least 80 % identical to a gene that exhibits increased or decreased expression in lung cancer samples. Lung cancer-associated polynucleotides and polypeptides are used for identifying a compound that modulates a lung cancer-associated polypeptide, for inhibiting proliferation of a lung cancer-associated cell to treat lung cancer in a patient and for treating a mammal having lung cancer by administering a modulatory compound identified. The methods are useful for treating lung cancer, such as small cell lung

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cancer, non-small cell lung cancer or other benign or precancerous lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and bronchiectasis. The genes, polynucleotides and polypeptides are useful for diagnostic purposes and as targets for screening for therapeutic compounds that modulate lung cancer, such as antibodies. Sequences ABX76124-ABX76474 represent lung cancer-associated polynucleotides of the invention.
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## SULT 4 172976 AA172976 standard; cDNA; 2081 BP.

72976 AAI72976 sta: AAI72976;

A172976;

(first entry)

21-AUG-2002

CJA8 preferred cDNA.

Gene, colorectal cancer, CGA7, CJA8; modulating protein; screening; drug candidate; vaccine; ss.

Homo sapiens.

y Location/Qualifiers 215..1528 /\*tag= a /product= "CJA8"

US2002042067-A1.

11-APR-2002.

08-MAY-2001; 2001US-0851588.

17-AUG-2000; 2000US-0642252. 06-SEP-2000; 2000US-0656002.

(MACK/) MACK D. (GISH/) GISH K C. (WILS/) WILSON K E. Mack D, Gish KC, Wilson KE;

WPI; 2002-453647/48. P-PSDB; AAG79359.

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Creening drug candidates for traating colorectal cancer, comprises

determining the effect of the candidate on the expression profile gene

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Claim 69; Fig 7; 40pp; English.

XX

The sequences given in AA12973-76 encode the colorectal cancer

Concerning proteins and have been mapped to chromosomes 2 (CGA)

and 11 (CAA8). These sequences may be used in the method of the
cancel modulating proteins and have been mapped to chromosomes 2 (CGA)

and 11 (CAA8). These sequences may be used in the method of the
canceling candidate on call that expression profile gene
canceling cAA7, CAA8 or fragments and determining the effect of the
canceling cAA7, CAA8 or tragments and determining the effect of the expression of the expression profile gene. The
canceling candidate on the expression of the expression profile gene
candidate on the expression of the expression profile gene
candidate on the expression of the expression profile gene
candidate colorectal cancer drug. An antibody to CGA7 or CUA8 can inhibit
can agent that can interfere with the binding of CGA7 or CUA8 can cancer. The
antibody or a fragment of it is used to localize a therapeutic group is
a colorectal cancer tissue, where the therapeutic group is a cyctoxic
cantibody or a fragment of it is used to localize a therapeutic group is
a colorectal cancer in a cell. Nucleic acid segments encoching CGA7 or
CUA8 are used to elicit an immune response. CGA7 or CUA8 is used to
colorectal cancer in a cell. Nucleic acid segments encoching CGA7 or
CUA8 are used to elicit an immune response. CGA7 or CUA8 is used to
determine the prognosis of an individual with colorectal cancer.

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human ovarian cancer marker OV86 2307 BP entry) standard; cDNA; (first encoding 11-DEC-2002 ABS76529; ABS76529 CDNA ESULT 5
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C ABS7
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T 11-L
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Huma
W Huma
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Human; ovarian cancer; marker; cancer; familial history; brain disorder; central nervous system disorder; bacterial meningitis; viral meningitis; Alzheimer's disease; Parkinson's disease; cerebral oedema; hydrocephalus; brain herniation; inflammation; encephalitis; testicular disorder; nontuberculous granulomatous orchitis; connective tissue disorder; heart disorder; ischaemic heart disease; atherosclerosis; neoplasm;

The present invention relates to a new method for assessing whether a patient is afflicted with ovarian cancer. The method involves comparing the expression level of a marker in a patient sample and the normal level of expression of the marker in a control non-ovarian cancer sample, where of expression of the marker in a control non-ovarian cancer sample, where the marker is selected from 363 cancer markers described in the characterising cancer, in detecting the presence of cancer as early as possible, and the recurrence of ovarian cancer. The method may also be of particular use with patients having an enhanced risk of developing ovarian cancer markers may be used in the management and treatment of e.g. brain and central nervous system disorders (e.g. bacterial and central nervous system disorders (e.g. brain enhingitis, Alzheimer's disease or Parkinson's disease), brain disorders (e.g. brain meningitis, Alzheimer's disease or Parkinson's disease), brain disorders (e.g. nontuberculous granulomatous orchitis), connective tissue disorders, or heart disorders (e.g. ischaemic heart disorders (e.g. ischaemic heart disorders (e.g. ischaemic heart disease or atherosclerosis). The compositions and methods may also be used in assessing the histological type of neoplasm associated with ovarian cancer, monitoring the progression of ovarian cancer, monitoring the progression of ovarian cancer, monitoring the progression of ovarian cancer. The metastasize, selecting a composition for inhibiting ovarian cancer or at risk of developing ovarian cancer or at risk of developing ovarian cancer markers concerned in the invention. Assessing whether a patient is afflicted with ovarian cancer, useful ir assessing the stage or progression of the disease, comprises comparing the expression level of a cancer marker in a sample from a patient and Kovatis SG; ), Mills GB; gene; Monahan JE, Gannavarapu M, Hoersch S, Kamatkar S, Ko Meyers RE, Morrisey MP, Olandt PJ, Sen A, Vieby PO, Bast RC, Lu K, Schmandt RE, Zhao X, Glatt K; marker; histological type; carcinogenic; ovarian cancer Disclosure; Page 438; 481pp; English 14-MAR-2001; 2001US-276025P. 14-MAR-2001; 2001US-276026P. 10-AUG-2001; 2001US-311732P. 19-SEP-2001; 2001US-323580P. 26-SEP-2001; 2001US-324967P. 26-SEP-2001; 2001US-325102P. 26-SEP-2001; 2001US-325102P. (MILL-) MILLENNIUM PHARM INC 14-MAR-2002; 2002WO-US07826 from a non cancer patient WPI; 2002-723277/78. P-PSDB; ABG96430. WO200271928-A2 Homo sapiens 19-SEP-2002 

614 G; 460 T; 31 other; BP; 555 A; 647 C; Sequence 2307

0000 Conservative: Mismatches: Length: Matches: Indels: 3.98e-209 2337.00 100.00% 100.00% 99.79% Percent Similarity: Best Local Similarity: Alignment Scores: Query Match:

US-09-607-745-2 (1-435) x ABS76529 (1-2307)

Db 1364 GGG  Qy 382 Gln  Db 1424 CAG  Qy 402 Val  Db 1484 GTI  Db 1544 GCG	ULT 6 64284 AAI64284 AAI64284; 07-MAY-20 Human ser Serine pr antinfla skin disc coagulati	Homo sa Key CDS DolyA_s	PD 10-JAN-2002 XX PF 08-JUN-2001 XX PR 30-JUN-2000 XX PA (ORTH ) ORTH XX PI DARROW AL, XX DR WPI, 2002-1, DR WPI, 2002-1, DR P-PSDB; AAG	XX  PT Useful for useful for production with the production with the production with the production with the production of the investigation of the production of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigation of the investigati
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alSerTrpGlyTyrGlyCysGlyGlyProSerThrProGlyValTyrThrLysValSer 421
                                                                                cion relates to an isolated and purified nucleic acid that serine protease called D-G protein. The activity of the protein vention may be described as cytostatic, antiinflammatory, gical and anticoagulation. The serine protease of the invention are of the trypsin/chymotrypsin-like (S1) serine protease family, an important role in processes such as digestion and y amplification cascades through the proteolytic activation of zymogen precursors. Protease D-G modulating compounds are usefuling a condition which is mediated by protease D-G, e.g. cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   id encoding a serine protease called D-G protein which is identifying modulators that are useful for treating a which is mediated by protease D-G, e.g. cancer, skin or neuropathic pain -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tease; D-G; human; zymogen; enzyme; cytostatic;
matory; dermatological; anticoagulation; cancer;
der; neuropathic pain; inflammatory disorder;
n diathesis; thrombosis; laundry detergent; skin care;
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skin disorders, neuropathic pain, inflammatory disorders, or coagulation diathesis/thrombosis. The polynucleotide encoding the protease is useful for identifying, detecting or isolating mutant forms of DNA molecules encoding the protease. The protease is useful for identifying modulators of the functional protease. The D-G protein can be used for formulation of compositions for laundry detergents and skin care products. Protease D-G gene therapy may be used to introduce protease D-G into the cells of target organisms. As the D-G protein is derived from a human, it is less likely to produce an allergic reaction in sensitive individuals when used in formulations for laundry detergents and skin care products. The current sequence represents the human serine protease D-G cDNA.
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/product= "Human seripancrin variant #1
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CAGTACGACAAACA

GlnTyrAspLysG]

rsLeuSerGlySe 

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ProArgvalvalG

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WPI; 2001-147177/15. P-PSDB; AAY72559.

serine procease Seripancrin, useful for treating is, arthritis, chronic obstructive pulmonary disease, tory disorders, stroke, angiogenesis and aberrant cancer, qsteoporosis, ¿ diabetes, inflammatory wound healing extracellular

45pp; English. Disclosure; Page 40-42;

of the invention are useful for treating and diagnosing diseases such as arthritis, chronic obstructive pulmonary disorder (COPD), cancer, osteoporosis, aberrant wound healing, angiogenesis, inflammatory disorders, diabetes, stroke and cardiovascular diseases. Seripancrin genes are useful in chromosome localisation studies, as tools for tissue expression studies and also in gene therapy. The polypeptides of the invention are used for identifying agonists and antagonists useful for treating conditions associated with seripancrin imbalance. These polypeptides are also useful as vaccines. The present sequence is a DNA coding for seripancrin variant #1 protein. The seripancrin gene is located on human chromosome 11q22-q23. The present invention relates to seripancrin polynuclectides, and polypeptides encoded by them. Seripancrin are members of serine protease family. This protein contains a transmembrane domain, a low density lipoprotein (LDL) domain, protease domain and a scavenger receptor cysteine-rich (SRCR) domain. The LDL and SRCR domains help to define the specificity of seripancrin's intra and intermolecular interactions. The polynucleotides and polypeptides of the invention are useful for treating and diagnosing diseases

A; 425 C; 407 G; 318 T; 0 other; Sequence 1479 BP; 329

Length:
Matches:
Conservative:
Mismatches:
Indels: 1.24e-208 2329.00 100.00% 100.00% 99.44% ercent Similarity: est Local Similarity: lignment Scores: ery Match: red. No.: core:

1479 432 0 0 0

x AAD02557 (1-1479) 3-09-607-745-2 (1-435)

GCAGTCCGCCTCTCCAAGGACCGATCCACACTGCAGGTGCTGGACTCGGCCACAGGGAAC 360 sPheAspAsnPheThrGluAlaLeuAlaGluThrAlaCysArgGln 140 STITCGACAACTICACAGAAGCICTCGCTGAGACAGCCTGTAGGCAG 420 ATGGGCTACAGCAGCAAACCCACTTTCAGAGCTGTGGAAATTGGCCCAGACCAGGATCTG 480 CTGGCGAGTATCATCATTGTTGTTGTCTCATCAAGGTGATTCTGGATAAATACTACTTC 180 uAspGluGluHisCysValLysSerPheProGluGlyProAlaVal 100 erLysProThrPheArgAlaValGluIleGlyProAspGlnAspLeu 160 agaccricagaaaggigggarcccardarcaracacracrgagg 120 40 9 80 erAspGlnProLeuAsnSerLeuAspValLysProLeuArgLysPro luThrPheArgLysValGly1leProlle1leAlaLeuLeuSer oLeuHisPhelleProArgiysGlnLeuCysAspGlyGluLeuAsp erLysAspArgSerThrLeuGlnValLeuAspSerAlaThrGlyAsn STGATCAACCTCTGAACAGCCTCGATGTCAAACCCCTGCGGCAAACCC TICTCCACTTCATCCCGAGGAAGCAGCTGTGTGTGTGACGGAGAGCTGGAC kedakedasedasersinersia kadaserri ese akadasesersedasis ellevalvalvalleulleLysvalileLeuAspLysTyrTyrPhe LeuAlaSerIleIl TrpPheSerAlaC 61 cerarcecearde CysProLeuGlyG] MetAspProAspS ArgileProMetG rercerregades AlaValArgLeuS MetGlyTyrSerS LeuCysGlyGlnP CTCTGCGGGCAGO ATGGATCCTGACA regriciciect 141 241 301 121 361 421 н 27 44 121 181 101 61 81

Homo sapiens

GlnGlyGluValThrGluLysMetMetCysAlaGlyIleProGluGlyGlyValAspThr 380 961 CCACTCTGGATCATTGGATGGGGCTTTACGAAGCAGAATGGAGGGAAGATGTCTGACATA 1020 1021 CTGCTGCAGGCGTCAGTCCAGGTCATTGACAGCACACGGTGCAATGCAGACGATGCGTAC 1080 260 200 220 099 720 840 300 900 ProLeuTrp11e11eGlyTrpG1yPheThrLysG1nAsnG1yG1yLysMetSerAsp11e 340 360 600 Human, artery; endothelium; umbilical; vein; aorta; pulmonary artery; bronchial epithelium; prostate; muscle; lung fibroblast; osteoblast; tumour; microarray; genome mapping; antibiotic; antiviral; antifungal; gene expression; gene; ss. 781 GACAAACTGGGCAGCTTCCCATCCCTGGCTGTGGCCAAGATCATCATCATTGAATTCAAC 301 SerglyThrValArgProlleCysLeuProPhePheAspGluGluLeuThrProAlaThr ProArgValValGlyGlyGluGluAlaSerValAspSerTrpProTrpGlnValSerIle 261 AspLysLeuGlySerPheProSerLeuAlaValAlaLysIleIleIleGluPheAsn IleValSerTrpGlyTyrGlyCysGlyGlyProSerThrProGlyValTyrThrLysVal 161 AspvalvalGluIleThrGluAsnSerGlnGluLeuArgMetArgAsnSerSerGlyPro GATGTTGTTGAAAATCACAGAAAACAGCCAGGAGCTTCGCATGCGGAACTCAAGTGGGGCCC CysLeuSerGlySerLeuValSerLeuHisCysLeuAlaCysGlyLysSerLeuLysThr 601 CCCCGTGTGGTGGGTGGGAGGAGGCCTCTGTGGGATTCTTGGCCTTGGCAGGTCAGCATC GlnTyrAspLysGlnHisValCysGlyGlySerIleLeuAspProHisTrpValLeuThr 661 CAGTACGACAACAGCACGTCTGTGGAGGAGCATCCTGGACCCCCCACTGGGTCCTCACG 241 AlaAlaHisCysPheArgLysHisThrAspValPheAsnTrpLysValArgAlaGlySer 721 GCAGCCCACTGCTTCAGGAAACATACCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCA ProMetTyrProLysAspAsnAspIleAlaLeuMetLysLeuGlnPheProLeuThrPhe TCAGGCACAGTCAGGCCCATCTGTCTTTTTTTTTAATGAGGAGCTCACTCCAGCCACC LeuLeuGlnAlaSerValGlnValIleAspSerThrArgCysAsnAlaAspAspAlaTyr Human gene expression profile polynucleotide SEQ ID NO 634. 1261 TCAGCCTATCTCAACTGGATCTACAATGTCTGGAAG 1296 SerAlaTyrLeuAsnTrpIleTyrAsnValTrpLys ВР ABZ35523 standard; cDNA; 2165 05-FEB-2003 (first entry) 1081 401 ABZ35523; 321 341 361 181 201 281 RESULT 8 q d 日 원 g ద Ωp à d Š  $\delta$  $\delta$ ò g à g ð ò  $\delta$  $\delta$  $\delta$ g ð

us-09-607-745-2.rng

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Disclosure, Page 759-760; 850pp; English
                               DIAGNOSTICS INC
                  2002WO-US08456.
                        20-MAR-2001; 2001US-276947P
                              (ORTH ) ORTHO CLINICAL
                                            WPI; 2002-740862/80
                                     Wang Y;
    WO200274979-A2
                 20-MAR-2002;
           26-SEP-2002
                                     Wan J,
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New gene expression profile generated from primary, endothelial, epithelial, and muscle cell types, useful for identifying disease pathologies involving alterations of gene expression, e.g. cancer

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The invention relates to a gene expression profile comprising one or more genes (ABZ34889-ABZ35692) and generated from a cell type. The cell type is a coronary artery endothelium, umbilical artery or vein endothelium, carmal microvascular endothelium, keratinocyte endothelium, menmeary epithelium, pulmonary artery cendthelium, momentium microvascular endothelium, prostate endothelium, prostate endothelium, renal epithelium, renal proximal tubule epithelium, canal cortical epithelium, renal proximal tubule epithelium, muscle, neonatal dermal fibroblast, pulmonary artery smooth muscle, messangial cells, skeletal muscle, astrocytes, dermal fibroblast, neural progenitor cells, skeletal muscle, astrocytes, cortic smooth muscle, mesangial cells, coronary artery smooth muscle, bronchial smooth muscle, uterine smooth muscle, lung fibroblast, corpusts of corpusts or prostate stromal cell. The gene expression profile is used for determining the level of RNA expression for a sample, determining the level of RNA expression. The gene or a protein expression profiles may provide meaningful information with respect to tumour type profiles may provide meaningful information with respect to tumour type and stage, treatment methods, and prognosis. The gene or protein expression profile may also be used for creating microarrays. The microarray is useful for genetic and physical mapping of erganisms, sequencing, genetic or medical diagnosis, genotyping of organisms, confirming cell or tissue identifications and in identifying promising antibiotics, antiviral or antifungal agents.

A; 623 C; 595 G; 445 T; 0 other; Sequence 2165 BP; 502

310 Arggarcergacagrearcacerergacacececeargreaacecergegeaaacec rAspGlnProLeuAsnSerLeuAspValLysProLeuArgLysPro elleValValLeulleLysVallleLeuAspLysTyrTyrPhe LeuCysGlyGlnProLeuHisPhelleProArglysGlnLeuCysAspGlyGluLeuAsp uThrPheArgLysValGlyIleProlleIleIleAlaLeuLeuSer 2165 435 0 0 1 Length:
Matches:
Conservative:
Mismatches:
Indels: 235523 (1-2165) 2.06e-208 2329.00 99.77% 99.77% 29.44% IS-09-607-745-2 (1-435) x AB CTCTGCGGGCAGCC 1 MetAspProAspSe CGTATCCCCATGGA LeuAlaSerIleIl CTGGCGAGTATCAT ArgileProMetGl score: Percent Similarity: Sest Local Similarity: Query Match: Alignment Scores: 370 490 21 430 41 61 . No. . red ð ð

Ö 2 ≿

 81 550	CysProLeuGlyGluAspGluGluHisCysValLysSerPheProGluGlyProAlaVal 100 
 101	AlavalArgLeuSerLysAspArgSerThrLeuGlnValLeuAspSerAlaThrGlyAsn 120 
 121	TrpPheSerAlaCysPheAspAsnPheThrGluAlaLeuAlaGluThrAlaCysArgGln 140 
 141	MetGlyTyrSerSerLysProThrPheArgAlaValGlulleGlyProAspGlnAspLeu 160 
 161	AspvalvaldlulleThrGluAsnSerGlnGlu-LeuArgMetArgAsnSerSerGlyPr 180 
 180	oCysLeuSerGlySerLeuValSerLeuHisCysLeuAlaCysGlyLysSerLeuLysTh 200 
 200	rProArgValValGlyGlyGluGluAlaSerValAspSerTrpProTrpGlnValSerIl 220 
220	eGlnTyraspLysGlnHisValCysGlyGlySerIleLeuAspProHisTrpValLeuTh 240 
 240	ralaalahisCysPheArgLysHisThrAspValPheAsnTrpLysValArgalaGlySe 260 
260	rAsplysLeuGlySerPheProSerLeuAlaValAlaLysIleIleIleIleGluPheAs 280 
280	nProMetTyrProLysAspAsnAspIleAlaLeuMetLysLeuGlnPheProLeuThrPh 300 
300	eSerGlyThrValArgProlleCysLeuProPhePheAspGluGluLeuThrProAlaTh 320 
320	rProLeuTrp11e11eG1yTrpG1yPheThrLysG1nAsnG1yG1yLysMetSerAsp11 340 
340	eLeuLeuGlnAlaSerValGlnValIleAspSerThrArgCysAsnAlaAspAspAlaTy 360 
360	rGlnGlyGluValThrGluLysMetMetCysAlaGlyIleProGluGlyGlyValAspTh 380 
380	rCysGlnGlyAspSerGlyGlyProLeuMetTyrGlnSerAspGlnTrpHisValValGl 400 
400	VIleValSerTrpGlyTyrGlyCysGlyGlyProSerThrProGlyValTyrThrLysVa 420 
420	120 ISeralaTyrLeuAsnTrpIleTyrAsnValTrpLysAlaGluLeu 435 

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AZ90471
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AAZ90471 standard; cDNA;

2070 BP

AAZ90471;

(first entry) 06-JUN-2000 Cancer specific gene (CSG) sequence (clone ID 1283171).

CSG; cancer specific gene; cancer; gynecologic cancer; ovarian; breast; endometrial; uterine; lung; cytotoxic; ss.

Homo sapiens.

WO200012758-A1

09-MAR-2000.

99WO-US19655. 01-SEP-1999; 98US-0098880. 02-SEP-1998;

(DIAD-) DIADEXUS LLC.

XMXXXXXXXXXXXXXXXHHHHXXXXIIII

Cafferkey R; Recipon H, Salceda S, Sun Y,

WPI; 2000-256657/22.

Diagnosing, staging, monitoring, imaging and treating cancer especially gynecological cancers e.g. breast, ovarian cancer and lung cancer, involves measuring cancer specific gene levels in cells and body fluids

Claim 9; Page 45-46; 58pp; English.

The invention relates to detecting, diagnosing metastasis and staging cancer by measuring levels of cancer specific genes (CSG) in cells, tissues or body fluids. Their remission and progression, decreases and increases in CSG levels, is also monitored, by periodic sample analysis. The methods are useful for detecting cancers, especially gynecologic cancers which include ovarian, breast, endometrial and uterine cancer and lung cancer. Antibodies against the CSGs labeled with paramagnetic ions or a radioisotope is useful for imaging cancer and when conjugated with a cytotoxic agent are useful for treating cancer. The present sequence represents a CSG sequence (clone ID: 1283171 and

Sequence 2070 BP; 473 A; 599 C; 577 G; 421 T; 0 other;

2070 Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: 5.7e-208 2324.00 99.77% 99.778 29.23% ore: rcent Similarity: st Local Similarity: ery Match: ignment Scores: No.:

-09-607-745-2 (1-435) x AAZ90471 (1-2070)

- 2 AspProAspSerAspGlnProLeuAsnSerLeuAspValLysProLeuArgLysProArg 21 223 GATCCTGACAGTG
- 283 ATCCCCATGGAGACCTTCAGAAAGGTGGGGATCCCCATCATCATAGCACTACTGAGCCTG 342 22 ileProMetGluThrPheArgLysValGlyIleProlleIleIleAlaLeuLeuSerLeu 41
- 343 degadrarcarcarrerrerrerrerreaderrerresarranaracractrecre 402 eValValValLeulleLysVallleLeuAspLysTyrTyrPheLeu 61 AlaSerileileil 42
- 62 CysGlyGlnProLeuHisPhelleProArgLysGlnLeuCysAspGlyGluLeuAspCys 81

Db	403 TGCGGGCAGCCTCTCCACTTCATCCCGAGGAAGCAGCTGTGTGACGGAGAGCTGGACGGAGAGCTGTGTGACGGAGAGCTGTGTGTG
Qy	2 ProLeuGlyGluAspGluGluHisCysValLysSerPheProGluGlyProAlaValAla 10
qq	3 CCCTTGGGGGAGGAGGAGGAGTGTGAAGAGCTTCCCCGAAGGGCCTGCAGTGGCA 52.
& &	102 ValArgLeuSerLysAspArgSerThrLeuGlnValLeuAspSerAlaThrGlyAsnTrp 121 
δŏ	22 pheSerAlaCysPheAspAsnPheThrGluAlaLeuAlaGluThrAlaCysArgGlnMet 14
qq	3 TICTCIGCCIGILITCGACACTICACAGAAGCICTCGCTGAGACAGCCTGTAGGCAGAIG 64
Š	142 GlyTyrSerSerLysProThrPheArgAlaValGluIleGlyProAspGlnAspLeuAsp 161
Db	CTACAGCAGCAAACCCACTTTCAGAGCTGTGGGGGCCCAGACCAGGATCTGGAT 70
Qy Dp	162 ValValGluIleThrGluAsnSerGlnGluLeuArgMetArgAsnSerSerGlyProCys 181
Š	rglyserleuvalserleuHisCysLeuAlaCysGlyLysSerleuLysThrPro 20
Ωb	
δλ	rgvalvalGlyGlyGluGluAlaSerValAspSerTrpProTrpGlnValSerIleGln 22
qq	GCATC
δ	222 TyraspLysGlnHisValCysGlyGlySerIleLeuAspProHisTrpValLeuThr-Al 241
qa	CGACAAACAGCACGTCTGTGGAGGGAGCATCCTGGACCCCCACTGGGTCCTCACG
ζŎ	41 aAlaHisCysPheArgLysHisThrAspValPheAsnTrpLysValArgAlaGlySerAs 261
අුග	43 AGCCCACTGCTTCAGGAAACATACCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGA 10
	261 pLysLeuGlySerPheProSerLeuAlaValAlaLysIleIleIleIleGluPheAsnPr 281
다. 기	003 CAAACTGGGCAGCTTCCCATCCCTGGCTGTGGCCAAGATCATCATCATTGAATTCAACCC 1
à i	81 OMETTYTPTOLYSASDASDASDILEAJALEUMETLYSLEUGINPheProleuThrPheSe 301
Db 1	FTACCCCAAAGACAATGACATCGCCCTCATGAAGCTGCAGTTCCCACTCACT
	301 rGlyThrValArgProIleCysLeuProPhePheAspGluGluLeuThrProAlaThrPr 321
DD T	123 AGGCACAGTCAGGCCCATCTGTCTGCCCTTCTTGATGAGGAGCTCACTCCAGCCACCC 11
OY Db 1	321 oLeuTrpileileGlyTrpGlyPheThrLysGlnAsnGlyGlyLysMetSerAspileLe 341 
λŏ	euGlnAlaSerValGlnValIleAspSerThrArgCysAsnAlaAspAspAlaTyr
Db 1	243 GCTGCAGGCGTCAGTCCAGGTCATTGACAGCACACGGTGCAATGCAGACGATGCGTACCA
Qy	GlyGluValThrGluLysMetMetCysAlaGlyIleProGluGlyGlyValAspT
Db 1	303 GGGGGAAGTCACCGAGAAGATGATGTGTGTGTGTTTTTTTT
δλ	381 sGlnGlyAspSerGlyGlyProLeuWetTyrGlnSerAspGlnTrpHisValValGlyIl 401
Db 3	363 ccadddidddddddddddddddddddddddddddddddd
Qy Db	401 eValSerTrpGlyTyrGlyCysGlyGlyProSerThrProGlyValTyrThrLysValSe 421
	421 rAlafyrLeuAsnTrpIleTyrAsnValTrpLysAlaGluLeu 435
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The invention relates to transmembrane serine proteases and their corresponding nucleotides and the protease domain of a type-II membrane-type serine protease (MTSP). MTSP is useful for identifying compounds that modulate or inhibits its proteolytic activity and for formulating a medicament for treating neoplastic disease. MTSP and its corresponding nucleotides are useful in preventing or treating tumours or cancers such as lung carcinoma, colon adenocarcinoma and ovarian carcinoma, in diagnostics and in hybridisation assays. MTSP is useful as a diagnostic marker for tumour development, growth and/or progression and as immunogens to generate antibodies that specifically bind to it. MTSP DNA is useful in a yeast two-hybrid system and in gene therapy. The present sequence is a DNA encoding human transmembrane protease, serine 4 (TMPRSS4) protein.
                                                                                                                                                         Human; transmembrane serine protease; membrane-type serine protease; MTSP; protease domain; neoplastic disease; tumour; cancer; cytostatic; lung carcinoma; colon adenocarcinoma; ovarian carcinoma; gene therapy; TMPRSS4; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             peptide comprising protease domain of type-II ofease or its catalytically active portion preventing cancer and tumor
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22-SEP-2000; 2000US-06579
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(WILS/) WILSON K
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candidate colorectal cancer drug. An antibody to CGA7 or CJA8 can inhibit the activity of CGA7 or CJA8, respectively, and is used to screen for an agent that can interfere with the binding of CGA7 or CJA8 to the antibody. The antibody can be used to treat colorectal cancer. The antibody or a fragment of it is used to localize a therapeutic group to a colorectal cancer tissue, where the therapeutic group is a cytotoxic agent or a radioisotope. Antisense molecules are used to inhibit colorectal cancer in a cell. Nucleic acid segments encoding CGA7 or CJA8 are used in a biochip. CGA7, CJA8 or a nucleic acid encoding it are used to elicit an immune response. CGA7 or CJA8 is used to determine the prognosis of an individual with colorectal cancer. Nucleic acid encoding CGA7 or CJA8 can be used in vaccines.
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                                                                                                                                                                                                                     The invention describes a method of diagnosing colorectal cancer comprising determining the expression of a gene encoding CJA8 or its fragment in a first colon tissue of an individual, and comparing the expression of the gene to the expression of the gene in normal tissue from the individual or in tissue from a second unaffected individual. A difference in the expression indicates that the first individual has colorectal cancer. The CJA8 genes and proteins are useful for diagnosing and prognosticating colorectal cancer. The methods are also useful for screening candidate bioactive agents that can modulate colorectal cancer, or for treating or inhibiting colorectal cancer in a patient e.g. by gene therapy. This sequence encodes the human colorectal cancer modulating protein CJA8.
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                                                                                         Diagnosing colorectal cancer comprises determining the expression of gene encoding CJA8 in a first colon tissue of a first individual, and comparing them to the expression of a gene encoding CJA8 in a second normal tissue.
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2137 BP AAD13114 standard; DNA;

AAD13114;

(first entry) 16-OCT-2001

Human membrane-type serine protease (MTSP) 3 DNA.

389

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329

41

449

81

Human, transmembrane serine protease, membrane-type serine protease, MTSP; protease domain; neoplastic disease; tumour; cancer; cytostatic; lung carcinoma; colon adenocarcinoma; ovarian carcinoma; gene therapy;

Homo sapiens

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Key
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Location/Qualifiers
261..1574
/*tag= a
/product= "Human transmembrane serine protease (MTSP) 3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to transmembrane serine proteases and their corresponding nucleotides and the protease domain of a type-II membrane-type serine protease (MTSP). MTSP is useful for identifying compounds that modulate or inhibits its proteolytic activity and for formulating a medicament for treating neoplastic disease. MTSP and its corresponding nucleotides are useful in preventing or treating tumours or cancers such as lung carcinoma, colon adenocarcinoma and ovarian carcinoma, in diagnostics and in hybridisation assays. MTSP is useful as a diagnostic marker for tumour development, growth and/or progression and as immunogens to generate antibodies that specifically bind to it. MTSP DNA is useful in a yeast two-hybrid system and in gene therapy. The present sequence is a DNA encoding human MTSP3
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22-JUN-2000; 2000US-0213124.
26-JUL-2000; 2000US-0220970.
08-SEP-2000; 2000US-0657986.
22-SEP-2000; 2000US-0234840.
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DY Obs. Aug. -2000 (first entry)

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Watanabe CK, Smith V, Gurney AL, ď Goddard ¥ Baker

Wood WI;

WPI; 2000-237871/20 P-PSDB; AAY99417.

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                                                                                                          AAA37022 to AAA37144 encode the new isolated human transmembrane, receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The transmembrane and receptor PRO proteins can be used for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions. The polypeptides and nucleotide sequences encoding then have various industrial applications, including uses as pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR primers and hybridisation probes used in the isolation of the PRO polypeptides from the present invention.
              New mammalian DNA sequences encoding transmembrane, receptor or secreted PRO polypeptides, useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AlaSerIleIleIleValValValLeuIleLysValIleLeuAspLysTyrTyrPheLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CysGlyGlnProLeuHisPhelleProArgLysGlnLeuCysAspGlyGluLeuAspCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             684 GIIGIIGAAAATCACAGAAAAAAAGCCAGGAGCTICGCAIGCGGAACTCAAGIGGGCCCTGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           519 GTCCGCCTCTCCAAGGACCGATCCACACTGCAGGTGCTGGACTCGGCCACACAGGGAACTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PheSerAlaCysPheAspAsnPheThrGluAlaLeuAlaGluThrAlaCysArgGlnMet
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IleProMetGluThrPheArgLysValGlyIleProIleIleIleAl
                                                                                                                                                                                                                                                                                     Sequence 2063 BP; 477 A; 591 C; 576 G; 419 T; 0 other;
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Mismatches:
Indels:
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Matches:
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                                                                                Claim 2; Fig 155; 773pp; English
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Pred. No.:
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              GTCTGTGGAGGGAGCATCCTGGACCCCCCACTGGGTCCTCACGGCA
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                                             gLysHisThrAspValPheAsnTrpLysValArgAlaGlySerAsp
                                                           SAAACATACCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGAC
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TyrasplysglnHis'
                                            AlaHisCysPheArg
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14-MAR-2000; 2000US-189328P.
15-MAR-2000; 2000W0-US06884.
21-MAR-2000; 2000US-190828P.
21-MAR-2000; 2000US-191048P.
21-MAR-2000; 2000US-191048P.
21-MAR-2000; 2000US-191048P.
29-MAR-2000; 2000US-193032P.
29-MAR-2000; 2000US-193032P.
29-MAR-2000; 2000US-193032P.
29-MAR-2000; 2000US-193032P.
30-MAR-2000; 2000US-194449P.
04-APR-2000; 2000US-194449P.
04-APR-2000; 2000US-19669P.
11-APR-2000; 2000US-196820P.
11-APR-2000; 2000US-196982P.
11-APR-2000; 2000US-196982P.
11-APR-2000; 2000US-196988P.
25-APR-2000; 2000US-199580P.
25-APR-2000; 2000US-199589P.
25-APR-2000; 2000US-199589P.
25-APR-2000; 2000US-199589P.
25-APR-2000; 2000US-199589P.
25-APR-2000; 2000US-199589P.
25-APR-2000; 2000US-199589P.
25-APR-2000; 2000US-199589P.
25-APR-2000; 2000WO-US13705.
22-MAY-2000; 2000WO-US13705.
22-AUG-2000; 2000WO-US3328.
24-AUG-2000; 2000WO-US3328.
20-DEC-2000; 2000WO-US33267.

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Sequences AAS45925-AAS46231 represent DNA molecules encoding and PCR primers for PRO polypeptides of the invention. The sequences of the invention can be used to detect the presence of a tumour in a mammal by comparing the level of expression of a PRO polypeptide in a test sample of cells from the animal and a control sample of normal cells, whereby a higher level of expression in the test sample indicates the presence of a tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats and rabbits but are preferably human. The polypeptides can be used to stimulate tumour necrosis factor (TNF) alpha release from human blood, when contacted with it. A specific polypeptide can be used to stimulate the proliferation or differentiation of chondrocyte cells. The PRO proteins can be used to determine the presence of tumours and also susceptibility to tumour development, particularly adrenal, lung, colon, breast, prostate, rectal, cervical, or liver tumours, in mammalian subjects. The oligonucleotide probes specific for the PRO nucleic acids can be used for genetic analysis of individuals with genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel nucleic acids encoding PRO polypeptides, used to diagnose the presence of tumours, such as prostate and breast tumours, in mammals and to screen for modulators of the compounds -
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Matches:
Conservative:
Mismatches:
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Pred. No.:
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PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; ss; dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha; blood; chondrocyte cell; cell proliferation; cell differentiation; colon; adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder; PCR primer.

polypeptide sequence #165

Human DNA encoding PRO

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(first

18-DEC-2001

AAS46089;

CDNA

standard;

AAS46089

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Percent Similarity: Best Local Similarity:

2000WO-US05601. 2000WO-US05841. 2000US-187202P. 2000US-186968P. 2000US-189320P.

01-MAR-2000; 02-MAR-2000; 03-MAR-2000; 06-MAR-2000; 14-MAR-2000;

28-FEB-2001; 2001WO-US06520.

WO200168848-A2

20-SEP-2001

sapiens

Homo

KUXHXMXSSSSSXOXZXOXAXAXAX

Gurney AL;

Godowski PJ, 1g Z;

Baker KP, Chen J, Desnoyers L, Goddard A, Gc Pan J, Smith V, Watanabe CK, Wood WI, Zhang

2001-602746/68.

WPI;

P-PSDB; AAU29188

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		oleuargi           crececa	salaLeuL          \GCACTAC	Lystyrt           AAATACT	oglyglub         ogagagg	AGGGCCTG	ralaThrG          sgccacaG	Alacysa         AGCCTGTA	AspGlnA          AGACCAGG	SerSerG         TCAAGTG	SerLeul         SAGCCTGA	Glnvals         scaggrca	TrpVall	ArgalaG         scgggcag	IleGluP          arrgaar	Probeut 	ThrProal	MetSerA          MATGTCTG	
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 		rLeuaspV            crccard	/Ileproi	eLysvali         CAAGGTGA	sbysglnL          saagcagc	LysserP           AAGAGCT	IGInVall         SCAGGTGC	alalarea           GCTCTCG	avalglui          rgrggaga	ileuArgM          scrrcgca	sCysLeuAlaCysGlyLysSerLeuLysThrPro 	AspserT           GATTCTT	rilerena          arccres	PheasnT	AlaLysi         GCCAAGA	MetLysL           ATGAAGC	PheAspG         TTTGATG	GlnAsnG        SCAGAATG	
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342 LeuGlnalaSerValGlnVallleAspSerThrArgCysAsnAlaAspAspAlaTyrGln 361

1224 CTGCAGGCGTCAGTCCAGGTCATTGACAGCACAGGTGCAATGCGTACCAG 1283

Qy

362 GlyGluValThrGluLysMetMetCysAlaGlyIleProGluGlyGlyValAspThrCys 381

1284 GGGAAGTCACCGAGAAGATGATGTGGCATCCGGAAGGGGTGTGGACCTGC 1343

Qy

382 GlnGlyAspSerGlyGlyProLeuMetTyrGlnSerAspGlnTrpHisValValGlyIle 401

1344 CAGGGTGACAGTGGGGCCCCTGATGTACCAATCTGACCAGTGGCATCTGGTGGCATC

Qy

402 ValSerTrpGlyTyrGlyCysGlyGlyProSerThrProGlyValTyrThrLysValSer 421

1404 GTTAGCTGGGGCTCGCGGGGCCCCGAGGACACCCCAGGAGTATACACCAAGGTCTCA 1463

Qy

422 AlaTyrLeuAsnTrpIleTyrAsnValTrpLysAlaGluLeu 435

Db

1464 GCCTATCTCAACTGGATCTACAATGTTCTGGAGCTGTCGAGCTCTCA 1463
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search completed: November 23, 2003, 08:06:43
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